

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Evans, Mark J.  
Matis, Louis A.  
Mueller, Eileen Elliott  
Nye, Steven H.  
Rollins, Scott  
Rother, Russell P.  
Springhorn, Jeremy P.  
Squinto, Stephen P.  
Thomas, Thomas C.  
Wilkins, James A.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
TREATMENT  
OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 26

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Seth A. Fidel  
(B) STREET: 25 Science Park (Alexion)  
(C) CITY: New Haven  
(D) STATE: Connecticut  
(E) COUNTRY: USA  
(F) ZIP: 06511

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.4Mb storage  
(B) COMPUTER: Macintosh Cetrus 610  
(C) OPERATING SYSTEM: System 7  
(D) SOFTWARE: WordPerfect 3.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/487,285  
(B) FILING DATE: June 7, 1995

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/236,208  
(B) FILING DATE: 02-MAY-1994

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seth A. Fidel.  
(B) REGISTRATION NUMBER: 38,449  
(C) REFERENCE/DOCKET NUMBER: ALX-152.1 CIP

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (203)776-1790  
(B) TELEFAX: (203)772-3655

- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 amino acids
    - (B) TYPE: Amino Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) MOLECULE TYPE
    - (A) DESCRIPTION: KSSKC peptide
  - (iii) HYPOTHETICAL: No
  - (iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Ile Asp His Gln Gly Thr Lys Ser Ser  
                                   5                                  10

Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser  
                                   15                                  20

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1676 Amino Acids
    - (B) TYPE: Amino Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (ii) MOLECULE TYPE
    - (A) DESCRIPTION: Pro-C5 Polypeptide
  - (iii) HYPOTHETICAL: No
  - (iv) ANTIISENSE: No
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Homo sapiens
  - (x) PUBLICATION INFORMATION:
    - (A) AUTHORS: Haviland, D.L.  
                   Haviland, J.C.  
                   Fleischer, D.T.  
                   Hunt, A.  
                   Wetsel, R.A.
    - (B) TITLE: Complete cDNA Sequence of Human Complement Pro-C5
    - (C) JOURNAL: Journal of Immunology
    - (D) VOLUME: 146
    - (F) PAGES: 362-368
    - (G) DATE: 1991

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

				Met	Gly	Leu	Leu	Gly	Ile	Leu	Cys	Phe	Leu
							-15					-10	
Ile	Phe	Leu	Gly	Lys	Thr	Trp	Gly	Gln	Glu	Gln	Thr	Tyr	Val
			-5				-1					5	
Ile	Ser	Ala	Pro	Lys	Ile	Phe	Arg	Val	Gly	Ala	Ser	Glu	Asn
			10					15					20
Ile	Val	Ile	Gln	Val	Tyr	Gly	Tyr	Thr	Glu	Ala	Phe	Asp	Ala
				25					30				
Thr	Ile	Ser	Ile	Lys	Ser	Tyr	Pro	Asp	Lys	Lys	Phe	Ser	Tyr
35					40					45			
Ser	Ser	Gly	His	Val	His	Leu	Ser	Ser	Glu	Asn	Lys	Phe	Gln
	50					55					60		
Asn	Ser	Ala	Ile	Leu	Thr	Ile	Gln	Pro	Lys	Gln	Leu	Pro	Gly
		65					70					75	
Gly	Gln	Asn	Pro	Val	Ser	Tyr	Val	Tyr	Leu	Glu	Val	Val	Ser
			80					85					90
Lys	His	Phe	Ser	Lys	Ser	Lys	Arg	Met	Pro	Ile	Thr	Tyr	Asp
				95					100				
Asn	Gly	Phe	Leu	Phe	Ile	His	Thr	Asp	Lys	Pro	Val	Tyr	Thr
105					110					115			
Pro	Asp	Gln	Ser	Val	Lys	Val	Arg	Val	Tyr	Ser	Leu	Asn	Asp
	120					125					130		
Asp	Leu	Lys	Pro	Ala	Lys	Arg	Glu	Thr	Val	Leu	Thr	Phe	Ile
		135					140					145	
Asp	Pro	Glu	Gly	Ser	Glu	Val	Asp	Met	Val	Glu	Glu	Ile	Asp
			150					155					160
His	Ile	Gly	Ile	Ile	Ser	Phe	Pro	Asp	Phe	Lys	Ile	Pro	Ser
				165					170				
Asn	Pro	Arg	Tyr	Gly	Met	Trp	Thr	Ile	Lys	Ala	Lys	Tyr	Lys
175					180					185			
Glu	Asp	Phe	Ser	Thr	Thr	Gly	Thr	Ala	Tyr	Phe	Glu	Val	Lys
	190					195					200		
Glu	Tyr	Val	Leu	Pro	His	Phe	Ser	Val	Ser	Ile	Glu	Pro	Glu

205					210					215				
Tyr	Asn	Phe	Ile	Gly	Tyr	Lys	Asn	Phe	Lys	Asn	Phe	Glu	Ile	
			220					225					230	
Thr	Ile	Lys	Ala	Arg	Tyr	Phe	Tyr	Asn	Lys	Val	Val	Thr	Glu	
				235					240					
Ala	Asp	Val	Tyr	Ile	Thr	Phe	Gly	Ile	Arg	Glu	Asp	Leu	Lys	
245					250					255				
Asp	Asp	Gln	Lys	Glu	Met	Met	Gln	Thr	Ala	Met	Gln	Asn	Thr	
	260					265					270			
Met	Leu	Ile	Asn	Gly	Ile	Ala	Gln	Val	Thr	Phe	Asp	Ser	Glu	
		275					280					285		
Thr	Ala	Val	Lys	Glu	Leu	Ser	Tyr	Tyr	Ser	Leu	Glu	Asp	Leu	
			290					295					300	
Asn	Asn	Lys	Tyr	Leu	Tyr	Ile	Ala	Val	Thr	Val	Ile	Glu	Ser	
				305					310					
Thr	Gly	Gly	Phe	Ser	Glu	Glu	Ala	Glu	Ile	Pro	Gly	Ile	Lys	
315					320					325				
Tyr	Val	Leu	Ser	Pro	Tyr	Lys	Leu	Asn	Leu	Val	Ala	Thr	Pro	
	330					335					340			
Leu	Phe	Leu	Lys	Pro	Gly	Ile	Pro	Tyr	Pro	Ile	Lys	Val	Gln	
		345					350					355		
Val	Lys	Asp	Ser	Leu	Asp	Gln	Leu	Val	Gly	Gly	Val	Pro	Val	
			360					365					370	
Ile	Leu	Asn	Ala	Gln	Thr	Ile	Asp	Val	Asn	Gln	Glu	Thr	Ser	
				375					380					
Asp	Leu	Asp	Pro	Ser	Lys	Ser	Val	Thr	Arg	Val	Asp	Asp	Gly	
385					390					395				
Val	Ala	Ser	Phe	Val	Leu	Asn	Leu	Pro	Ser	Gly	Val	Thr	Val	
	400					405					410			
Leu	Glu	Phe	Asn	Val	Lys	Thr	Asp	Ala	Pro	Asp	Leu	Pro	Glu	
		415					420					425		
Glu	Asn	Gln	Ala	Arg	Glu	Gly	Tyr	Arg	Ala	Ile	Ala	Tyr	Ser	
			430					435					440	
Ser	Leu	Ser	Gln	Ser	Tyr	Leu	Tyr	Ile	Asp	Trp	Thr	Asp	Asn	

				445						450				
His	Lys	Ala	Leu	Leu	Val	Gly	Glu	His	Leu	Asn	Ile	Ile	Val	
455					460					465				
Thr	Pro	Lys	Ser	Pro	Tyr	Ile	Asp	Lys	Ile	Thr	His	Tyr	Asn	
	470					475					480			
Tyr	Leu	Ile	Leu	Ser	Lys	Gly	Lys	Ile	Ile	His	Phe	Gly	Thr	
		485					490					495		
Arg	Glu	Lys	Phe	Ser	Asp	Ala	Ser	Tyr	Gln	Ser	Ile	Asn	Ile	
			500					505					510	
Pro	Val	Thr	Gln	Asn	Met	Val	Pro	Ser	Ser	Arg	Leu	Leu	Val	
				515					520					
Tyr	Tyr	Ile	Val	Thr	Gly	Glu	Gln	Thr	Ala	Glu	Leu	Val	Ser	
525					530					535				
Asp	Ser	Val	Trp	Leu	Asn	Ile	Glu	Glu	Lys	Cys	Gly	Asn	Gln	
	540					545					550			
Leu	Gln	Val	His	Leu	Ser	Pro	Asp	Ala	Asp	Ala	Tyr	Ser	Pro	
		555					560					565		
Gly	Gln	Thr	Val	Ser	Leu	Asn	Met	Ala	Thr	Gly	Met	Asp	Ser	
			570					575					580	
Trp	Val	Ala	Leu	Ala	Ala	Val	Asp	Ser	Ala	Val	Tyr	Gly	Val	
				585					590					
Gln	Arg	Gly	Ala	Lys	Lys	Pro	Leu	Glu	Arg	Val	Phe	Gln	Phe	
595					600					605				
Leu	Glu	Lys	Ser	Asp	Leu	Gly	Cys	Gly	Ala	Gly	Gly	Gly	Leu	
	610					615					620			
Asn	Asn	Ala	Asn	Val	Phe	His	Leu	Ala	Gly	Leu	Thr	Phe	Leu	
		625					630					635		
Thr	Asn	Ala	Asn	Ala	Asp	Asp	Ser	Gln	Glu	Asn	Asp	Glu	Pro	
			640					645					650	
Cys	Lys	Glu	Ile	Leu	Arg	Pro	Arg	Arg	Thr	Leu	Gln	Lys	Lys	
				655					660					
Ile	Glu	Glu	Ile	Ala	Ala	Lys	Tyr	Lys	His	Ser	Val	Val	Lys	
665					670					675				
Lys	Cys	Cys	Tyr	Asp	Gly	Ala	Cys	Val	Asn	Asn	Asp	Glu	Thr	

680				685				690					
Cys	Glu	Gln	Arg	Ala	Ala	Arg	Ile	Ser	Leu	Gly	Pro	Arg	Cys
		695					700					705	
Ile	Lys	Ala	Phe	Thr	Glu	Cys	Cys	Val	Val	Ala	Ser	Gln	Leu
			710					715					720
Arg	Ala	Asn	Ile	Ser	His	Lys	Asp	Met	Gln	Leu	Gly	Arg	Leu
				725					730				
His	Met	Lys	Thr	Leu	Leu	Pro	Val	Ser	Lys	Pro	Glu	Ile	Arg
735					740					745			
Ser	Tyr	Phe	Pro	Glu	Ser	Trp	Leu	Trp	Glu	Val	His	Leu	Val
	750					755					760		
Pro	Arg	Arg	Lys	Gln	Leu	Gln	Phe	Ala	Leu	Pro	Asp	Ser	Leu
		765					770					775	
Thr	Thr	Trp	Glu	Ile	Gln	Gly	Ile	Gly	Ile	Ser	Asn	Thr	Gly
			780					785					790
Ile	Cys	Val	Ala	Asp	Thr	Val	Lys	Ala	Lys	Val	Phe	Lys	Asp
				795					800				
Val	Phe	Leu	Glu	Met	Asn	Ile	Pro	Tyr	Ser	Val	Val	Arg	Gly
805					810					815			
Glu	Gln	Ile	Gln	Leu	Lys	Gly	Thr	Val	Tyr	Asn	Tyr	Arg	Thr
	820					825					830		
Ser	Gly	Met	Gln	Phe	Cys	Val	Lys	Met	Ser	Ala	Val	Glu	Gly
		835					840					845	
Ile	Cys	Thr	Ser	Glu	Ser	Pro	Val	Ile	Asp	His	Gln	Gly	Thr
			850					855					860
Lys	Ser	Ser	Lys	Cys	Val	Arg	Gln	Lys	Val	Glu	Gly	Ser	Ser
				865					870				
Ser	His	Leu	Val	Thr	Phe	Thr	Val	Leu	Pro	Leu	Glu	Ile	Gly
875					880					885			
Leu	His	Asn	Ile	Asn	Phe	Ser	Leu	Glu	Thr	Trp	Phe	Gly	Lys
	890					895					900		
Glu	Ile	Leu	Val	Lys	Thr	Leu	Arg	Val	Val	Pro	Glu	Gly	Val
		905					910					915	

Lys	Arg	Glu	Ser	Tyr	Ser	Gly	Val	Thr	Leu	Asp	Pro	Arg	Gly	920	925	930
Ile	Tyr	Gly	Thr	Ile	Ser	Arg	Arg	Lys	Glu	Phe	Pro	Tyr	Arg	935	940	
Ile	Pro	Leu	Asp	Leu	Val	Pro	Lys	Thr	Glu	Ile	Lys	Arg	Ile	945	950	955
Leu	Ser	Val	Lys	Gly	Leu	Leu	Val	Gly	Glu	Ile	Leu	Ser	Ala	960	965	970
Val	Leu	Ser	Gln	Glu	Gly	Ile	Asn	Ile	Leu	Thr	His	Leu	Pro	975	980	985
Lys	Gly	Ser	Ala	Glu	Ala	Glu	Leu	Met	Ser	Val	Val	Pro	Val	990	995	1000
Phe	Tyr	Val	Phe	His	Tyr	Leu	Glu	Thr	Gly	Asn	His	Trp	Asn	1005	1010	
Ile	Phe	His	Ser	Asp	Pro	Leu	Ile	Glu	Lys	Gln	Lys	Leu	Lys	1015	1020	1025
Lys	Lys	Leu	Lys	Glu	Gly	Met	Leu	Ser	Ile	Met	Ser	Tyr	Arg	1030	1035	1040
Asn	Ala	Asp	Tyr	Ser	Tyr	Ser	Val	Trp	Lys	Gly	Gly	Ser	Ala	1045	1050	1055
Ser	Thr	Trp	Leu	Thr	Ala	Phe	Ala	Leu	Arg	Val	Leu	Gly	Gln	1060	1065	1070
Val	Asn	Lys	Tyr	Val	Glu	Gln	Asn	Gln	Asn	Ser	Ile	Cys	Asn	1075	1080	
Ser	Leu	Leu	Trp	Leu	Val	Glu	Asn	Tyr	Gln	Leu	Asp	Asn	Gly	1085	1090	1095
Ser	Phe	Lys	Glu	Asn	Ser	Gln	Tyr	Gln	Pro	Ile	Lys	Leu	Gln	1100	1105	1110
Gly	Thr	Leu	Pro	Val	Glu	Ala	Arg	Glu	Asn	Ser	Leu	Tyr	Leu	1115	1120	1125
Thr	Ala	Phe	Thr	Val	Ile	Gly	Ile	Arg	Lys	Ala	Phe	Asp	Ile	1130	1135	1140
Cys	Pro	Leu	Val	Lys	Ile	Asp	Thr	Ala	Leu	Ile	Lys	Ala	Asp	1145	1150	

Asn	Phe	Leu	Leu	Glu	Asn	Thr	Leu	Pro	Ala	Gln	Ser	Thr	Phe
1155					1160					1165			
Thr	Leu	Ala	Ile	Ser	Ala	Tyr	Ala	Leu	Ser	Leu	Gly	Asp	Lys
	1170					1175					1180		
Thr	His	Pro	Gln	Phe	Arg	Ser	Ile	Val	Ser	Ala	Leu	Lys	Arg
		1185					1190					1195	
Glu	Ala	Leu	Val	Lys	Gly	Asn	Pro	Pro	Ile	Tyr	Arg	Phe	Trp
			1200					1205					1210
Lys	Asp	Asn	Leu	Gln	His	Lys	Asp	Ser	Ser	Val	Pro	Asn	Thr
				1215						1220			
Gly	Thr	Ala	Arg	Met	Val	Glu	Thr	Thr	Ala	Tyr	Ala	Leu	Leu
1225					1230					1235			
Thr	Ser	Leu	Asn	Leu	Lys	Asp	Ile	Asn	Tyr	Val	Asn	Pro	Val
	1240					1245					1250		
Ile	Lys	Trp	Leu	Ser	Glu	Glu	Gln	Arg	Tyr	Gly	Gly	Gly	Phe
		1255					1260					1265	
Tyr	Ser	Thr	Gln	Asp	Thr	Ile	Asn	Ala	Ile	Glu	Gly	Leu	Thr
			1270					1275					1280
Glu	Tyr	Ser	Leu	Leu	Val	Lys	Gln	Leu	Arg	Leu	Ser	Met	Asp
				1285					1290				
Ile	Asp	Val	Ser	Tyr	Lys	His	Lys	Gly	Ala	Leu	His	Asn	Tyr
1295					1300					1305			
Lys	Met	Thr	Asp	Lys	Asn	Phe	Leu	Gly	Arg	Pro	Val	Glu	Val
	1310					1315					1320		
Leu	Leu	Asn	Asp	Asp	Leu	Ile	Val	Ser	Thr	Gly	Phe	Gly	Ser
		1325					1330					1335	
Gly	Leu	Ala	Thr	Val	His	Val	Thr	Thr	Val	Val	His	Lys	Thr
			1340					1345					1350
Ser	Thr	Ser	Glu	Glu	Val	Cys	Ser	Phe	Tyr	Leu	Lys	Ile	Asp
				1355					1360				
Thr	Gln	Asp	Ile	Glu	Ala	Ser	His	Tyr	Arg	Gly	Tyr	Gly	Asn
1365					1370					1375			
Ser	Asp	Tyr	Lys	Arg	Ile	Val	Ala	Cys	Ala	Ser	Tyr	Lys	Pro
	1380					1385					1390		



Ser	Arg	Glu	Glu	Ser	Ser	Ser	Gly	Ser	Ser	His	Ala	Val	Met
		1395					1400					1405	
Asp	Ile	Ser	Leu	Pro	Thr	Gly	Ile	Ser	Ala	Asn	Glu	Glu	Asp
			1410					1415					1420
Leu	Lys	Ala	Leu	Val	Glu	Gly	Val	Asp	Gln	Leu	Phe	Thr	Asp
				1425					1430				
Tyr	Gln	Ile	Lys	Asp	Gly	His	Val	Ile	Leu	Gln	Leu	Asn	Ser
1435					1440					1445			
Ile	Pro	Ser	Ser	Asp	Phe	Leu	Cys	Val	Arg	Phe	Arg	Ile	Phe
	1450					1455					1460		
Glu	Leu	Phe	Glu	Val	Gly	Phe	Leu	Ser	Pro	Ala	Thr	Phe	Thr
		1465					1470					1475	
Val	Tyr	Glu	Tyr	His	Arg	Pro	Asp	Lys	Gln	Cys	Thr	Met	Phe
			1480					1485					1490
Tyr	Ser	Thr	Ser	Asn	Ile	Lys	Ile	Gln	Lys	Val	Cys	Glu	Gly
				1495					1500				
Ala	Ala	Cys	Lys	Cys	Val	Glu	Ala	Asp	Cys	Gly	Gln	Met	Gln
1505					1510					1515			
Glu	Glu	Leu	Asp	Leu	Thr	Ile	Ser	Ala	Glu	Thr	Arg	Lys	Gln
	1520					1525					1530		
Thr	Ala	Cys	Lys	Pro	Glu	Ile	Ala	Tyr	Ala	Tyr	Lys	Val	Ser
		1535					1540					1545	
Ile	Thr	Ser	Ile	Thr	Val	Glu	Asn	Val	Phe	Val	Lys	Tyr	Lys
			1550					1555					1560
Ala	Thr	Leu	Leu	Asp	Ile	Tyr	Lys	Thr	Gly	Glu	Ala	Val	Ala
				1565					1570				
Glu	Lys	Asp	Ser	Glu	Ile	Thr	Phe	Ile	Lys	Lys	Val	Thr	Cys
1575					1580					1585			
Thr	Asn	Ala	Glu	Leu	Val	Lys	Gly	Arg	Gln	Tyr	Leu	Ile	Met
	1590					1595					1600		
Gly	Lys	Glu	Ala	Leu	Gln	Ile	Lys	Tyr	Asn	Phe	Ser	Phe	Arg
		1605					1610					1615	
Tyr	Ile	Tyr	Pro	Leu	Asp	Ser	Leu	Thr	Trp	Ile	Glu	Tyr	Trp
			1620					1625					1630

Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala  
 1635 1640

Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys  
 1645 1650 1655

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4059 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Apex-1 Eukaryotic  
Expression Vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACGCGTTGAC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG	50
GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG	100
TAAATGGCCC CGCCTGGCTG ACCGCCCAAC GACCCCCGCC CATTGACGTC	150
AATAATGACG TATGTTCCCA TAGTAACGCC AATAGGGACT TTCCATTGAC	200
GTCAATGGGT GGACTATTTA CGGTAAACTG CCCACTTGGC AGTACATCAA	250
GTGTATCATA TGCCAAGTAC GCCCCCTATT GACGTCAATG ACGGTAAATG	300
GCCCGCCTGG CATTATGCCC AGTACATGAC CTTATGGGAC TTTCCTACTT	350
GGCAGTACAT CTACGTATTA GTCATCGCTA TTACCATGGT GATGCGGTTT	400
TGGCAGTACA TCAATGGGCG TGGATAGCGG TTTGACTCAC GGGGATTTCC	450
AAGTCTCCAC CCCATTGACG TCAATGGGAG TTTGTTTTTG CACCAAATC	500
AACGGGACTT TCCAAAATGT CGTAACAACT CCGCCCCATT GACGCAAATG	550
GGCGGTAGGC GTGTACGGTG GGAGGTCTAT ATAAGCAGAG CTCGTTTAGT	600
GAACCGTCAG AATTCTGTTG GGCTCGCGGT TGATTACAAA CTCTTCGCGG	650
TCTTTCCAGT ACTCTTGGAT CGGAAACCCG TCGGCCTCCG AACGGTACTC	700
CGCCACCGAG GGACCTGAGC GAGTCCGCAT CGACCGGATC GGAAAACCTC	750
TCGACTGTTG GGGTGAGTAC TCCCTCTCAA AAGCGGGCAT GACTTCTGCG	800

CTAAGATTGT	CAGTTTCCAA	AAACGAGGAG	GATTTGATAT	TCACCTGGCC	850
CGCGGTGATG	CCTTTGAGGG	TGGCCGCGTC	CATCTGGTCA	GAAAAGACAA	900
TCTTTTTGTT	GTCAAGCTTG	AGGTGTGGCA	GGCTTGAGAT	CTGGCCATAC	950
ACTTGAGTGA	CAATGACATC	CACTTTGCCT	TTCTCTCCAC	AGGTGTCCAC	1000
TCCCAGGTCC	AACTGCAGGT	CGACCGGCTT	GGTACCGAGC	TCGGATCCAC	1050
TAGTAACGGC	CGCCAGTGTG	CTGGAATTCT	GCAGATATCC	ATCACACTGG	1100
CGGCCGCTCG	AGCATGCATC	TAGAACTTGT	TTATTGCAGC	TTATAATGGT	1150
TACAAATAAA	GCAATAGCAT	CACAAATTTT	ACAAATAAAG	CATTTTTTTT	1200
ACTGCATTCT	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	TCTTATCATG	1250
TCTGGATCGA	TCCCGCCATG	GTATCAACGC	CATATTTCTA	TTTACAGTAG	1300
GGACCTCTTC	GTTGTGTAGG	TACCGCTGTA	TTCCTAGGGA	AATAGTAGAG	1350
GCACCTTGAA	CTGTCTGCAT	CAGCCATATA	GCCCCGCTG	TTCGACTTAC	1400
AAACACAGGC	ACAGTACTGA	CAAACCCATA	CACCTCCTCT	GAAATACCCA	1450
TAGTTGCTAG	GGCTGTCTCC	GAATCATTAA	CACCCTCCAA	AGTCAGAGCT	1500
GTAATTTTCG	CATCAAGGGC	AGCGAGGGCT	TCTCCAGATA	AAATAGCTTC	1550
TGCCGAGAGT	CCCGTAAGGG	TAGACACTTC	AGCTAATCCC	TCGATGAGGT	1600
CTACTAGAAT	AGTCAGTGCG	GCTCCCATT	TGAAAATTCA	CTTACTTGAT	1650
CAGCTTCAGA	AGATGGCGGA	GGCCTCCAA	CACAGTAATT	TTCTCCCGA	1700
CTCTTAAAAT	AGAAAATGTC	AAGTCAGTTA	AGCAGGAAGT	GGACTAACTG	1750
ACGCAGCTGG	CCGTGCGACA	TCCTCTTTTA	ATTAGTTGCT	AGGCAACGCC	1800
CTCCAGAGGG	CGTGTGGTTT	TGCAAGAGGA	AGCAAAAGCC	TCTCCACCCA	1850
GGCCTAGAAT	GTTTCCACCC	AATCATTACT	ATGACAACAG	CTGTTTTTTT	1900
TAGTATTAAG	CAGAGGCCGG	GGACCCCTGG	GCCCGCTTAC	TCTGGAGAAA	1950
AAGAAGAGAG	GCATTGTAGA	GGCTTCCAGA	GGCAACTTGT	CAAAACAGGA	2000
CTGCTTCTAT	TTCTGTCACA	CTGTCTGGCC	CTGTCACAAG	GTCCAGCACC	2050

TCCATACCCC	CTTTAATAAG	CAGTTTGGGA	ACGGGTGCGG	GTCTTACTCC	2100
GCCCATCCCG	CCCCTAACTC	CGCCAGTTC	CGCCATTCT	CCGCCCCATG	2150
GCTGACTAAT	TTTTTTTATT	TATGCAGAGG	CCGAGGCCGC	CTCGGCCTCT	2200
GAGCTATTCC	AGAAGTAGTG	AGGAGGCTTT	TTTGGAGGCC	TAGGCTTTTG	2250
CAAAAAGGAG	CTCCCAGCAA	AAGGCCAGGA	ACCGTAAAAA	GGCCGCGTTG	2300
CTGGCGTTTT	TCCATAGGCT	CCGCCCCCCT	GACGAGCATC	ACAAAAATCG	2350
ACGCTCAAGT	CAGAGGTGGC	GAAACCCGAC	AGGACTATAA	AGATACCAGG	2400
CGTTTCCCCC	TGGAAGCTCC	CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	2450
CTTACCGGAT	ACCTGTCCGC	CTTTCTCCCT	TCGGGAAGCG	TGGCGCTTTC	2500
TCAATGCTCA	CGCTGTAGGT	ATCTCAGTTC	GGTGTAGGTC	GTTCGCTCCA	2550
AGCTGGGCTG	TGTGCACGAA	CCCCCGTTC	AGCCCGACCG	CTGCGCCTTA	2600
TCCGGTAACT	ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	2650
ACTGGCAGCA	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	TATGTAGGCG	2700
GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA	ACTACGGCTA	CACTAGAAGG	2750
ACAGTATTTG	GTATCTGCGC	TCTGCTGAAG	CCAGTTACCT	TCGGAAAAAG	2800
AGTTGGTAGC	TCTTGATCCG	GCAAACAAAC	CACCGCTGGT	AGCGGTGGTT	2850
TTTTTGTTTG	CAAGCAGCAG	ATTACGCGCA	GAAAAAAAGG	ATCTCAAGAA	2900
GATCCTTTGA	TCTTTTCTAC	GGGTCTGAC	GCTCAGTGGA	ACGAAAACCTC	2950
ACGTTAAGGG	ATTTTGGTCA	TGAGATTATC	AAAAAGGATC	TTCACCTAGA	3000
TCCTTTTAAA	TTAAAAATGA	AGTTTTTAAAT	CAATCTAAAG	TATATATGAG	3050
TAAACTTGGT	CTGACAGTTA	CCAATGCTTA	ATCAGTGAGG	CACCTATCTC	3100
AGCGATCTGT	CTATTTCTGT	CATCCATAGT	TGCCTGACTC	CCCGTCGTGT	3150
AGATAACTAC	GATACGGGAG	GGCTTACCAT	CTGGCCCCAG	TGCTGCAATG	3200
ATACCGCGAG	ACCCACGCTC	ACCGGCTCCA	GATTTATCAG	CAATAAACCA	3250
GCCAGCCGGA	AGGGCCGAGC	GCAGAAGTGG	TCCTGCAACT	TTATCCGCCT	3300
CCATCCAGTC	TATTAATTGT	TGCCGGAAG	CTAGAGTAAG	TAGTTCGCCA	3350

GTTAATAGTT TGC	GCAACGT TGT	TGCCATT GCT	TACAGGCA TCG	TGGTGTC	3400
ACGCTCGTCG TTT	GGTATGG CTT	CATTTCAG CT	CCGGTTCC CA	ACGATCAA	3450
GGCGAGTTAC AT	GATCCCC AT	GTTGTGCA AA	AAAAGCGGT	TAGCTCCTTC	3500
GGTCCTCCGA TCG	TTGTCAG AAG	TAAGTTG GCC	GCAGTGT TAT	CACTCAT	3550
GGTTATGGCA GCA	CTGCATA ATT	CTCTTAC TG	TTCATGCCA	TCCGTAAGAT	3600
GCTTTTCTGT GAC	TGGTGAG TAC	TCAACCA AG	TCATTCTG	AGAATAGTGT	3650
ATGCGGCGAC CG	AGTTGCTC TT	GCCCGGCG	TCAATACGGG	ATAATACCGC	3700
GCCACATAGC AGA	ACTTTAA AAG	TGCTCAT	CATTGGAAAA	CGTTCTTCGG	3750
GGCGAAAAC	CTCAAGGATC	TTACCGCTGT	TGAGATCCAG	TTCGATGTAA	3800
CCCCTCGTG CAC	CCCACTG AT	CTTCAGCA	TCTTTTACTT	TCACCAGCGT	3850
TTCTGGGTGA GCA	AAAAACAG	GAAGGCAAAA	TGCCGCAAAA	AAGGGAATAA	3900
GGGCGACACG GAA	ATGTTGA AT	ACTCATAC	TCTTCCTTTT	TCAATATTAT	3950
TGAAGCATTT AT	CAGGGTTA	TTGTCTCATG	AGCGGATACA	TATTTGAATG	4000
TATTTAGAAA AAT	AACA AAA	TAGGGGTTCC	GCGCACATTT	CCCCGAAAAG	4050
TGCCACCTG					4059

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8540 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Circular

## (ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Apex-3P Eukaryotic  
Expression Vector

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCAATA CAA	AACAAA GCG	CCCCCTCG	TACCAGCGAA	GAAGGGGCAG	50
AGATGCCGTA GTC	AGGTTTA GT	TCGTCCGG	CGGCGGGGGA	TCTGTATGGT	100
GCACTCTCAG TACA	ATCTGC TCT	GATGCCG	CATAGTTAAG	CCAGTATCTG	150

CTCCCTGCTT	GTGTGTTGGA	GGTCGCTGAG	TAGTGCGCGA	GCAAAATTTA	200
AGCTACAACA	AGGCAAGGCT	TGACCGACAA	TTGCATGAAG	AATCTGCTTA	250
GGGTAGGCG	TTTTGCGCTG	CTTCGCGATG	TACGGGCCAG	ATATACGCGT	300
TGACATTGAT	TATTGACTAG	TTATTAATAG	TAATCAATTA	CGGGGTCATT	350
AGTTCATAGC	CCATATATGG	AGTTCCGCGT	TACATAACTT	ACGGTAAATG	400
GCCCGCCTGG	CTGACCGCCC	AACGACCCCC	GCCCATTGAC	GTCAATAATG	450
ACGTATGTTC	CCATAGTAAC	GCCAATAGGG	ACTTTCCATT	GACGTCAATG	500
GGTGGACTAT	TTACGGTAAA	CTGCCCACTT	GGCAGTACAT	CAAGTGTATC	550
ATATGCCAAG	TACGCCCCCT	ATTGACGTCA	ATGACGGTAA	ATGGCCCCGCC	600
TGGCATTATG	CCCAGTACAT	GACCTTATGG	GACTTTCCTA	CTTGGCAGTA	650
CATCTACGTA	TTAGTCATCG	CTATTACCAT	GGTGATGCGG	TTTTGGCAGT	700
ACATCAATGG	GCGTGGATAG	CGGTTTGACT	CACGGGGATT	TCCAAGTCTC	750
CACCCCATTG	ACGTCAATGG	GAGTTTGT'TT	TGGCACCAAA	ATCAACGGGA	800
CTTTCCAAAA	TGTCGTAACA	ACTCCGCCCC	ATTGACGCAA	ATGGGCGGTA	850
GGCGTG'TACG	GTGGGAGGTC	TATATAAGCA	GAGCTCGTTT	AGTGAACCGT	900
CAGAATTCTG	TTGGGCTCGC	GGTTGATTAC	AAACTCTTCG	CGGTCTTTCC	950
AGTACTCTTG	GATCGGAAAC	CCGTCGGCCT	CCGAACGGTA	CTCCGCCACC	1000
GAGGGACCTG	AGCGAGTCCG	CATCGACCGG	ATCGGAAAAC	CTCTCGACTG	1050
TTGGGGTGAG	TACTCCCTCT	CAAAAGCGGG	CATGACTTCT	GCGCTAAGAT	1100
TGTCAGTTTC	CAAAAACGAG	GAGGATT'TGA	TATTCACCTG	GCCCGCGGTG	1150
ATGCCTTTGA	GGGTGGCCGC	GTCCATCTGG	TCAGAAAAGA	CAATCTTTTT	1200
GTTGTCAAGC	TTGAGGTGTG	GCAGGCTTGA	GATCTGGCCA	TACACTTGAG	1250
TGACAATGAC	ATCCACTTTG	CCTTTCTCTC	CACAGGTGTC	CACTCCCAGG	1300
TCCAAGTGCA	GGTCGACCGG	CTTGGTACCG	AGCTCGGATC	CTCTAGAGTC	1350
GACCTGCAGG	CATGCAAGCT	TGGCACTGGC	CGTCGTTTTA	CAACGTCGTG	1400
ACTGGGAAAA	CCCTGGCGTT	ACCCAAC'TTA	ATCGCCTTGC	AGCACATCCC	1450

CCTTTCGCCA GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCCAGACAT 1500  
 GATAAGATAC ATTGATGAGT TTGGACAAAC CACAAC TAGA ATGCAGTGAA 1550  
 AAAAATGCTT TATTTGTGAA ATTTGTGATG CTATTGCTTT ATTTGTAACC 1600  
 ATTATAAGCT GCAATAAACA AGTTAACAAC AACAAATTGCA TTCATTTTAT 1650  
 GTTTCAGGTT CAGGGGGAGG TGTGGGAGGT TTTTAAAGC AAGTAAAACC 1700  
 TCTACAAATG TGGTATGGCT GATTATGATC CCCAGGAAGC TCCTCTGTGT 1750  
 CCTCATAAAC CCTAACCTCC TCTACTTGAG AGGACATTCC AATCATAGGC 1800  
 TGCCCATCCA CCCTCTGTGT CCTCCTGTTA ATTAGGTCAC TTAACAAAAA 1850  
 GGAAATTGGG TAGGGGT TTT TCACAGACCG CTTTCTAAGG GTAATTTTAA 1900  
 AATATCTGGG AAGTCCCTTC CACTGCTGTG TTCCAGAAGT GTTGGTAAAC 1950  
 AGCCCACAAA TGTCAACAGC AGAAACATAC AAGCTGTCAG CTTTGCACAA 2000  
 GGGCCCAACA CCCTGCTCAT CAAGAAGCAC TGTGGTTGCT GTGT TAGTAA 2050  
 TGTGCAAAAC AGGAGGCACA TTTTCCCCAC CTGTGTAGGT TCCAAAATAT 2100  
 CTAGTGTTTT CATT TTTACT TGGATCAGGA ACCCAGCACT CCACTGGATA 2150  
 AGCATTATCC TTATCCAAAA CAGCCTTG TG GTCAGTGTTT ATCTGCTGAC 2200  
 TGTCAACTGT AGCATTTTTT GGGGTACAG TTTGAGCAGG ATATTTGGTC 2250  
 CTGTAGTTTG CTAACACACC CTGCAGCTCC AAAGGTTCCC CACCAACAGC 2300  
 AAAAAAATGA AAATTTGACC CTTGAATGGG TTTTCCAGCA CCATTTTCAT 2350  
 GAGTTTTTTT TGTCCCTGAA TGCAAGTTTA ACATAGCAGT TACCCCAATA 2400  
 ACCTCAGTTT TAACAGTAAC AGCTTCCCAC ATCAAAATAT TTCCACAGGT 2450  
 TAAGTCCTCA TTTGTAGAAT TCGCCAGCAC AGTGGTCGAC CCTGTGGATG 2500  
 TGTGTCACTT AGGGTGTGGA AAGTCCCCAG GCTCCCCAGC AGGCAGAAGT 2550  
 ATGCAAAGCA TGCATCTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC 2600  
 AGGCTCCCCA GCAGGCAGAA GTATGCAAAG CATGCATCTC AATTAGTCAG 2650  
 CAACCATAGT CCCGCCCTA ACTCCGCCCA TCCCGCCCCT AACTCCGCC 2700

AGTTCCGCCC ATTCTCCGCC CCATGGCTGA CTAATTTTTT TTATTTATGC 2750  
 AGAGGCCGAG GCCGCCTCGG CCTCTGAGCT ATTCCAGAAG TAGTGAGGAG 2800  
 GCTTTTTTGG AGGCCTAGGC TTTTGCAAAA GCTTACCATG ACCGAGTACA 2850  
 AGCCCACGGT GCGCCTCGCC ACCCGCGACG ACGTCCCCCG GGCCGTACGC 2900  
 ACCCTCGCCG CCGCGTTCGC CGACTACCCC GCCACGCGCC ACACCGTCGA 2950  
 CCCGGACCGC CACATCGAGC GGGTCACCGA GCTGCAAGAA CTCTTCCTCA 3000  
 CGCGCGTCGG GCTCGACATC GGCAAGGTGT GGGTCGCGGA CGACGGCGCC 3050  
 GCGGTGGCGG TCTGGACCAC GCCGGAGAGC GTCGAAGCGG GGGCGGTGTT 3100  
 CGCCGAGATC GGCCCGCGCA TGGCCGAGTT GAGCGGTTCC CGGCTGGCCG 3150  
 CGCAGCAACA GATGGAAGGC CTCCTGGCGC CGCACCGGCC CAAGGAGCCC 3200  
 GCGTGGTTCC TGGCCACCGT CGGCGTCTCG CCCGACCACC AGGGCAAGGG 3250  
 TCTGGGCAGC GCCGTCGTGC TCCCCGGAGT GGAGGCGGCC GAGCGCGCCG 3300  
 GGGTGCCCGC CTTCTGAGG ACCTCCGCGC CCCGCAACCT CCCCTTCTAC 3350  
 GAGCGGCTCG GCTTCACCGT CACCGCCGAC GTCGAGTGCC CGAAGGACCG 3400  
 CGCGACCTGG TGCATGACCC GCAAGCCCGG TGCCTGACGC CCGCCCCACG 3450  
 ACCCGCAGCG CCCGACCGAA AGGAGCGCAC GACCCCATGC ATCGATAAAA 3500  
 TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGGAATGA AAGACCCAC 3550  
 CTGTAGGTTT GGCAAGCTAG AACTTGTTTA TTGCAGCTTA TAATGGTTAC 3600  
 AAATAAAGCA ATAGCATCAC AAATTTACAA AATAAAGCAT TTTTTTCACT 3650  
 GCATTCTAGT TGTGGTTTGT CCAAACATCAT CAATGTATCT TATCATGTCT 3700  
 GGATCGATCC CGCCATGGTA TCAACGCCAT ATTTCTATTT ACAGTAGGGA 3750  
 CCTCTTCGTT GTGTAGGTAC CCCGGGTTCG AAATCGAATT CGCCAATGAC 3800  
 AAGACGCTGG GCGGGGTTTG TGTCATCATA GAACTAAAGA CATGCAAATA 3850  
 TATTTCTTCC GGGGACACCG CCAGCAAACG CGAGCAACGG GCCACGGGGA 3900  
 TGAAGCAGCC CGGCGGCACC TCGCTAACGG ATTCACCACT CCAAGAATTG 3950  
 GAGCCAATCA ATTCTTGCGG AGAACTGTGA ATGCGCAAAC CAACCCTTGG 4000



CAGAACATAT CCATCGCGTC CGCCATCTCC AGCAGCCGCA CGCGGCGCAT 4050  
 CTCGGGGCCG ACGCGCTGGG CTACGTCTTG CTGGCGTTCG CGACGCGAGG 4100  
 CTGGATGGCC TTCCCCATTA TGATTCTTCT CGCTTCCGGC GGCATCGGGA 4150  
 TGCCCGCGTT GCAGGCCATG CTGTCCAGGC AGGTAGATGA CGACCATCAG 4200  
 GGACAGCTTC AAGGATCGCT CGCGGCTCTT ACCAGCGCCA GCAAAAGGCC 4250  
 AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTTCATA GGCTCCGCCC 4300  
 CCCTGACGAG CATCACAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC 4350  
 CGACAGGACT ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG 4400  
 CGCTCTCCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT 4450  
 CCCTTCGGGA AGCGTGGCGC TTTCTCATAG CTCACGCTGT AGGTATCTCA 4500  
 GTTCGGTGTA GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC 4550  
 GTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA 4600  
 CCCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA 4650  
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 TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTAAAA ATGAAGTTTT 5000  
 AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG 5050  
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 GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC 5550  
 TTA CTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA 5600  
 ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC 5650  
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 AACACCTTCT CGCGTTGGAA AACATTAGCG ACATTTACCT GGTGAGCAAT 6300  
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 GAGCAACCAG CAGGAAAAGG ACAAGCAGCG AAAATTCACG CCCCTTGGG 6400  
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 TTAGGATAGC ATATACTACC CAGATATAGA TTAGGATAGC ATATGCTACC 6550

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 GATAGCATAT GCTACCCGGA TACAGATTAG GATAGCATAT ACTACCCAGA 6850  
 TATAGATTAG GATAGCATAT GCTACCCAGA TATAGATTAG GATAGCCTAT 6900  
 GCTACCCAGA TATAAATTAG GATAGCATAT ACTACCCAGA TATAGATTAG 6950  
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 TATAGATTAG GATAGCATAT GCTATCCAGA TATTTGGGTA GTATATGCTA 7050  
 CCCATGGCAA CATTAGCCCA CCGTGCTCTC AGCGACCTCG TGAATATGAG 7100  
 GACCAACAAC CCTGTGCTTG GCGCTCAGGC GCAAGTGTGT GTAATTTGTC 7150  
 CTCCAGATCG CAGCAATCGC GCCCCTATCT TGGCCCGCCC ACCTACTTAT 7200  
 GCAGGTATTC CCCGGGGTGC CATTAGTGGT TTTGTGGGCA AGTGGTTTGA 7250  
 CCGCAGTGGT TAGCGGGGTT ACAATCAGCC AAGTTATTAC ACCCTTATTT 7300  
 TACAGTCCAA AACCGCAGGG CGGCGTGTGG GGGCTGACGC GTGCCCCCAC 7350  
 TCCACAATTT CAAAAAAAG AGTGGCCACT TGTCTTTGTT TATGGGCCCC 7400  
 ATTGGCGTGG AGCCCCGTTT AATTTTCGGG GGTGTTAGAG ACAACCAGTG 7450  
 GAGTCCGCTG CTGTCGGCGT CCACTCTCTT TCCCCTTGTT ACAAATAGAG 7500  
 TGTAACAACA TGGTTCACCT GTCTTGGTCC CTGCCTGGGA CACATCTTAA 7550  
 TAACCCCAAG ATCATATTGC ACTAGGATTA TGTGTTGCCC ATAGCCATAA 7600  
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 ATTTCTATTG TTAAAGATAT TCAGAATGTT TCATTCCTAC ACTAGTATTT 7700  
 ATTGCCCAAG GGGTTTGTGA GGGTTATATT GGTGTCATAG CACAATGCCA 7750  
 CCACTGAACC CCCCGTCCAA ATTTTATTCT GGGGGCGTCA CCTGAAACCT 7800

TGTTTTTCGAG CACCTCACAT ACACCTTACT GTTCACAACCT CAGCAGTTAT 7850  
 TCTATTAGCT AAACGAAGGA GAATGAAGAA GCAGGCGAAG ATTCAGGAGA 7900  
 GTTCACTGCC CGCTCCTTGA TCTTCAGCCA CTGCCCTTGT GACTAAAATG 7950  
 GTTCACTACC CTCGTGGAAT CCTGACCCCA TGTAATAAAA ACCGTGACAG 8000  
 CTCATGGGGT GGGAGATATC GCTGTTTCCTT AGGACCCTTT TACTAACCCT 8050  
 AATTCGATAG CATATGCTTC CCGTTGGGTA ACATATGCTA TTGAATTAGG 8100  
 GTTAGTCTGG ATAGTATATA CTACTACCCG GGAAGCATAT GCTACCCGTT 8150  
 TAGGGTTAAC AAGGGGGCCT TATAAACACT ATTGCTAATG CCCTCTTGAG 8200  
 GGTCCGCTTA TCGGTAGCTA CACAGGCCCC TCTGATTGAC GTTGGTGTAG 8250  
 CCTCCCGTAG TCTTCCTGGG CCCCTGGGAG GTACATGTCC CCCAGCATTG 8300  
 GTGTAAGAGC TTCAGCCAAG AGTTACACAT AAAGGCAATG TTGTGTTGCA 8350  
 GTCCACAGAC TGCAAAGTCT GCTCCAGGAT GAAAGCCACT CAGTGTTGGC 8400  
 AAATGTGCAC ATCCATTTAT AAGGATGTCA ACTACAGTCA GAGAACCCCT 8450  
 TTGTGTTTGG TCCCCCCCCG TGTCACATGT GGAACAGGGC CCAGTTGGCA 8500  
 AGTTGTACCA ACCAACTGAA GGGATTACAT GCACTGCCCC 8540

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer UDEC690

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCTGCAGG ACATCCAGAT GACTCAGTCT

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer UDEC395

## (iii) HYPOTHETICAL: No

## (iv) ANTI-SENSE: Yes

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA

30

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1M1 scFv (murine)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GCC GAC ATC CAG ATG ACT CAG TCT CCA 30

Met Ala Asp Ile Gln Met Thr Gln Ser Pro

1

5

10

GCT TCA CTG TCT GCA TCT GTG GGA GAA ACT 60

Ala Ser Leu Ser Ala Ser Val Gly Glu Thr

15

20

GTC ACC ATC ACA TGT GGA GCA AGT GAG AAT 90

Val Thr Ile Thr Cys Gly Ala Ser Glu Asn

25

30

ATT TAC GGT GCT TTA AAT TGG TAT CAG CGG 120

Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg

35

40

AAA CAG GGA AAA TCT CCT CAG CTC CTG ATC 150

Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile

45

50

TAT GGT GCA ACC AAC TTG GCA GAT GGC ATG 180

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met

55

60

TCA	TCG	AGG	TTC	AGT	GGC	AGT	GGA	TCT	GGT	210
Ser	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	70
				65						
AGA	CAG	TAT	TAT	CTC	AAG	ATC	AGT	AGC	CTG	240
Arg	Gln	Tyr	Tyr	Leu	Lys	Ile	Ser	Ser	Leu	80
				75						
CAT	CCT	GAC	GAT	GTT	GCA	ACG	TAT	TAC	TGT	270
His	Pro	Asp	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	90
				85						
CAA	AAT	GTG	TTA	AAT	ACT	CCT	CTC	ACG	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	100
				95						
GGT	GCT	GGG	ACC	AAG	TTG	GAG	CTG	AAA	CGG	330
Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	110
				105						
ACC	GGA	GGT	GGC	GGG	TCG	GGT	GGC	GGG	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	120
				115						
TCG	GGT	GGC	GGA	GGG	TCG	CAG	GTT	CAG	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	130
				125						
CAG	CAG	TCT	GGA	GCC	GAG	CTG	ATG	AAG	CCT	420
Gln	Gln	Ser	Gly	Ala	Glu	Leu	Met	Lys	Pro	140
				135						
GGG	GCC	TCA	GTG	AAG	ATG	TCC	TGC	AAG	GCT	450
Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	150
				145						
ACT	GGC	TAC	ATA	TTC	AGT	AAC	TAC	TGG	ATA	480
Thr	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	160
				155						
CAG	TGG	ATA	AAG	CAG	AGG	CCT	GGA	CAT	GGC	510
Gln	Trp	Ile	Lys	Gln	Arg	Pro	Gly	His	Gly	170
				165						
CTT	GAG	TGG	ATT	GGT	GAG	ATT	TTA	CCT	GGA	540
Leu	Glu	Trp	Ile	Gly	Glu	Ile	Leu	Pro	Gly	180
				175						
AGT	GGT	TCT	ACT	GAG	TAC	ACT	GAG	AAC	TTC	570
Ser	Gly	Ser	Thr	Glu	Tyr	Thr	Glu	Asn	Phe	

				185					190	
AAG	GAC	AAG	GCC	GCA	TTC	ACT	GCA	GAT	ACA	600
Lys	Asp	Lys	Ala	Ala	Phe	Thr	Ala	Asp	Thr	
				195					200	
TCC	TCC	AAC	ACA	GCC	TAC	ATG	CAA	CTC	AGC	630
Ser	Ser	Asn	Thr	Ala	Tyr	Met	Gln	Leu	Ser	
				205					210	
AGC	CTG	ACA	TCA	GAG	GAC	TCT	GCC	GTC	TAT	660
Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	
				215					220	
TAC	TGT	GCA	AGA	TAT	TTC	TTC	GGT	AGT	AGC	690
Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	Gly	Ser	Ser	
				225					230	
CCC	AAC	TGG	TAC	TTC	GAT	GTC	TGG	GGC	GCA	720
Pro	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Ala	
				235					240	
GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	TGA		747
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser			
				245						

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv CB (humanized)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	GCC	GAT	ATC	CAG	ATG	ACC	CAG	TCC	CCG	30
Met	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	
1				5					10	
TCC	TCC	CTG	TCC	GCC	TCT	GTG	GGC	GAT	AGG	60
Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
				15					20	
GTC	ACC	ATC	ACC	TGC	GGC	GCC	AGC	GAA	AAC	90
Val	Thr	Ile	Thr	Cys	Gly	Ala	Ser	Glu	Asn	
				25					30	

ATC	TAT	GGC	GCG	CTG	AAC	TGG	TAT	CAA	CGT	120
Ile	Tyr	Gly	Ala	Leu	Asn	Trp	Tyr	Gln	Arg	
				35					40	
AAA	CCT	GGG	AAA	GCT	CCG	AAG	CTT	CTG	ATT	150
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
				45					50	
TAC	GGT	GCG	ACG	AAC	CTG	GCA	GAT	GGA	GTC	180
Tyr	Gly	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	
				55					60	
CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	
ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	
CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	
GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	
ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	
TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	
GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	
GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	
AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	



CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	
CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	
TCT	GGT	AGC	ACC	GAA	TAT	ACC	GAA	AAT	TTT	570
Ser	Gly	Ser	Thr	Glu	Tyr	Thr	Glu	Asn	Phe	
				185					190	
AAA	GAC	CGT	GTT	ACT	ATG	ACG	CGT	GAC	ACT	600
Lys	Asp	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	
				195					200	
TCG	ACT	AGT	ACA	GTA	TAC	ATG	GAG	CTC	TCC	630
Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	
				205					210	
AGC	CTG	CGA	TCG	GAG	GAC	ACG	GCC	GTC	TAT	660
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	
				215					220	
TAT	TGC	GCG	CGT	TAT	TTT	TTT	GGT	TCT	AGC	690
Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	Gly	Ser	Ser	
				225					230	
CCG	AAT	TGG	TAT	TTT	GAT	GTT	TGG	GGT	CAA	720
Pro	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	
				235					240	
GGA	ACC	CTG	GTC	ACT	GTC	TCG	AGC	TGA		747
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
				245						

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGC AGT GGA TCT GGT AGA CAG TAT TAT CTC 300  
Gly Ser Gly Ser Gly Arg Gln Tyr Tyr Leu  
70 75

AAG	ATC	AGT	AGC	CTG	CAT	CCT	GAC	GAT	GTT	330
Lys	Ile	Ser	Ser	Leu	His	Pro	Asp	Asp	Val	
				80					85	
GCA	ACG	TAT	TAC	TGT	CAA	AAT	GTG	TTA	AAT	360
Ala	Thr	Tyr	Tyr	Cys	Gln	Asn	Val	Leu	Asn	
				90					95	
ACT	CCT	CTC	ACG	TTC	GGT	GCT	GGG	ACC	AAG	390
Thr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	
				100					105	
TTG	GAG	CTG	AAA	CGA	ACT	GTG	GCT	GCA	CCA	420
Leu	Glu	Leu	Lys	Arg	Thr	Val	Ala	Ala	Pro	
				110					115	
TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAT	GAG	450
Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	
				120					125	
CAG	TTG	AAA	TCT	GGA	ACT	GCC	TCT	GTT	GTG	480
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	
				130					135	
TGC	CTG	CTG	AAT	AAC	TTC	TAT	CCC	AGA	GAG	510
Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	
				140					145	
GCC	AAA	GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	540
Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	
				150					155	
CTC	CAA	TCG	GGT	AAC	TCC	CAG	GAG	AGT	GTC	570
Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	
				160					165	
ACA	GAG	CAG	GAC	AGC	AAG	GAC	AGC	ACC	TAC	600
Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	
				170					175	
AGC	CTC	AGC	AGC	ACC	CTG	ACG	CTG	AGC	AAA	630
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
				180					185	
GCA	GAC	TAC	GAG	AAA	CAC	AAA	GTC	TAC	GCC	660
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	
				190					195	
TGC	GAA	GTC	ACC	CAT	CAG	GGC	CTG	AGC	TCG	690
Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	
				200					205	

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720  
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu  
                   210                  215

TGT TAG 726  
 Cys

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1M1 VH +HuG1 (chimeric Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG AAA TGG AGC TGG GTT ATT CTC TTC CTC 30  
 Met Lys Trp Ser Trp Val Ile Leu Phe Leu  
                   -15                  -10

CTG TCA GTA ACT GCA GGT GTC CAC TCC CAG 60  
 Leu Ser Val Thr Ala Gly Val His Ser Gln  
                   -5                  1

GTT CAG CTG CAG CAG TCT GGA GCT GAG CTG 90  
 Val Gln Leu Gln Gln Ser Gly Ala Glu Leu  
                   5                  10

ATG AAG CCT GGG GCC TCA GTG AAG ATG TCC 120  
 Met Lys Pro Gly Ala Ser Val Lys Met Ser  
                   15                  20

TGC AAG GCT ACT GGC TAC ATA TTC AGT AAC 150  
 Cys Lys Ala Thr Gly Tyr Ile Phe Ser Asn  
                   25                  30

TAC TGG ATA CAG TGG ATA AAG CAG AGG CCT 180  
 Tyr Trp Ile Gln Trp Ile Lys Gln Arg Pro  
                   35                  40

GGA CAT GGC CTT GAG TGG ATT GGT GAG ATT 210  
 Gly His Gly Leu Glu Trp Ile Gly Glu Ile  
                   45                  50

TTA	CCT	GGA	AGT	GGT	TCT	ACT	GAG	TAC	ACT	240
Leu	Pro	Gly	Ser	Gly	Ser	Thr	Glu	Tyr	Thr	
			55					60		
GAG	AAC	TTC	AAG	GAC	AAG	GCC	GCA	TTC	ACT	270
Glu	Asn	Phe	Lys	Asp	Lys	Ala	Ala	Phe	Thr	
			65					70		
GCA	GAT	ACA	TCC	TCC	AAC	ACA	GCC	TAC	ATG	300
Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Tyr	Met	
			75					80		
CAA	CTC	AGC	AGC	CTG	ACA	TCA	GAG	GAC	TCT	330
Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	
			85					90		
GCC	GTC	TAT	TAC	TGT	GCA	AGA	TAT	TTC	TTC	360
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	
			95					100		
GGT	AGT	AGC	CCC	AAC	TGG	TAC	TTC	GAT	GTC	390
Gly	Ser	Ser	Pro	Asn	Trp	Tyr	Phe	Asp	Val	
			105					110		
TGG	GGC	GCA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	420
Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	
			115					120		
TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	450
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
			125					130		
CCC	CTG	GCG	CCC	TCC	TCC	AAG	AGC	ACC	TCT	480
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	
			135					140		
GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	GTC	510
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	
			145					150		
AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	540
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
			155					160		
TCG	TGG	AAC	TCA	GGC	GCC	CTG	ACC	AGC	GGC	570
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	
			165					170		
GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	600
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
			175					180		

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660  
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
 195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690  
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
 205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720  
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
 215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750  
 Pro Lys Ser Cys Asp Lys Thr His Thr  
 225

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VH + IGHRL (Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30  
 Met Lys Trp Ser Trp Val Ile Leu Phe Leu  
 -15 -10

CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60  
 Leu Ser Val Thr Ala Gly Val His Ser Gln  
 -5 1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90  
 Val Gln Leu Val Gln Ser Gly Ala Glu Val  
 5 10

AAG AAG CCA GGG GCC TCA GTC AAA GTG TCC 120  
 Lys Lys Pro Gly Ala Ser Val Lys Val Ser  
 15 20

TGT	AAA	GCT	AGC	GGC	TAT	ATT	TTT	TCT	AAT	150
Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Ser	Asn	
			25					30		
TAT	TGG	ATT	CAA	TGG	GTG	CGT	CAG	GCC	CCC	180
Tyr	Trp	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	
			35					40		
GGG	CAG	GGC	CTG	GAA	TGG	ATG	GGT	GAG	ATC	210
Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	
			45					50		
TTA	CCG	GGC	TCT	GGT	AGC	ACC	GAA	TAT	GCC	240
Leu	Pro	Gly	Ser	Gly	Ser	Thr	Glu	Tyr	Ala	
			55					60		
CAA	AAA	TTC	CAG	GGC	CGT	GTT	ACT	ATG	ACT	270
Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	
			65					70		
GCG	GAC	ACT	TCG	ACT	AGT	ACA	GCC	TAC	ATG	300
Ala	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	Met	
			75					80		
GAG	CTC	TCC	AGC	CTG	CGA	TCG	GAG	GAC	ACG	330
Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	
			85					90		
GCC	GTC	TAT	TAT	TGC	GCG	CGT	TAT	TTT	TTT	360
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	
			95					100		
GGT	TCT	AGC	CCG	AAT	TGG	TAT	TTT	GAT	GTT	390
Gly	Ser	Ser	Pro	Asn	Trp	Tyr	Phe	Asp	Val	
			105					110		
TGG	GGT	CAA	GGA	ACC	CTG	GTC	ACT	GTC	TCG	420
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
			115					120		
AGC	GCC	TCC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	450
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
			125					130		
CCC	CTG	GCG	CCC	TCC	TCC	AAG	AGC	ACC	TCT	480
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	
			135					140		
GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	GTC	510
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	
			145					150		

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540  
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 155 160

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
 165 170

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600  
 Val His Thr Phe Pro Ala Val Leu Gln Ser  
 175 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660  
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
 195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690  
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
 205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720  
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
 215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750  
 Pro Lys Ser Cys Asp Lys Thr His Thr  
 225 230

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VH + IGHRLC (Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30  
 Met Lys Trp Ser Trp Val Ile Leu Phe Leu  
 -15 -10



CTG	TCA	GTA	ACT	GCC	GGC	GTC	CAC	TCC	CAA	60
Leu	Ser	Val	Thr	Ala	Gly	Val	His	Ser	Gln	
				-5					1	
GTC	CAA	CTG	GTG	CAA	TCC	GGC	GCC	GAG	GTC	90
Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	
			5					10		
AAG	AAG	CCA	GGG	GCC	TCA	GTC	AAA	GTG	TCC	120
Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	
			15					20		
TGT	AAA	GCT	AGC	GGC	TAT	ATT	TTT	TCT	AAT	150
Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Ser	Asn	
			25					30		
TAT	TGG	ATT	CAA	TGG	GTG	CGT	CAG	GCC	CCC	180
Tyr	Trp	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	
			35					40		
GGG	CAG	GGC	CTG	GAA	TGG	ATG	GGT	GAG	ATC	210
Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	
			45					50		
TTA	CCG	GGC	TCT	GGT	AGC	ACC	GAA	TAT	ACC	240
Leu	Pro	Gly	Ser	Gly	Ser	Thr	Glu	Tyr	Thr	
			55					60		
GAA	AAT	TTT	AAA	GAC	CGT	GTT	ACT	ATG	ACG	270
Glu	Asn	Phe	Lys	Asp	Arg	Val	Thr	Met	Thr	
			65					70		
CGT	GAC	ACT	TCG	ACT	AGT	ACA	GTA	TAC	ATG	300
Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr	Met	
			75					80		
GAG	CTC	TCC	AGC	CTG	CGA	TCG	GAG	GAC	ACG	330
Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	
			85					90		
GCC	GTC	TAT	TAT	TGC	GCG	CGT	TAT	TTT	TTT	360
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	
			95					100		
GGT	TCT	AGC	CCG	AAT	TGG	TAT	TTT	GAT	GTT	390
Gly	Ser	Ser	Pro	Asn	Trp	Tyr	Phe	Asp	Val	
			105					110		
TGG	GGT	CAA	GGA	ACC	CTG	GTC	ACT	GTC	TCG	420
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
			115					120		

AGC	GCC	TCC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	450
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
			125					130		
CCC	CTG	GCG	CCC	TCC	TCC	AAG	AGC	ACC	TCT	480
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	
			135					140		
GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	GTC	510
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	
			145					150		
AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	540
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
			155					160		
TCG	TGG	AAC	TCA	GGC	GCC	CTG	ACC	AGC	GGC	570
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	
			165					170		
GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	600
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
			175					180		
TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	630
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	
			185					190		
ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG	660
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	
			195					200		
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	690
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
			205					210		
AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA	GTT	GAG	720
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	
			215					220		
CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TAA	750
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr		
			225					230		

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VL +KLV56  
(Humanized light chain)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30  
Met Gly Ile Gln Gly Gly Ser Val Leu Phe  
-25 -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60  
Gly Leu Leu Leu Val Leu Ala Val Phe Cys  
-15 -10

CAT TCA GGT CAT AGC CTG CAG GAT ATC CAG 90  
His Ser Gly His Ser Leu Gln Asp Ile Gln  
-5 1 5

ATG ACC CAG TCC CCG TCC TCC CTG TCC GCC 120  
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
10 15

TCT GTG GGC GAT AGG GTC ACC ATC ACC TGC 150  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys  
20 25

GGC GCC AGC GAA AAC ATC TAT GGC GCG CTG 180  
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu  
30 35

AAC TGG TAT CAA CGT AAA CCT GGG AAA GCT 210  
Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala  
40 45

CCG AAG CTT CTG ATT TAC GGT GCG ACG AAC 240  
Pro Lys Leu Leu Ile Tyr Gly Ala Thr Asn  
50 55

CTG GCA GAT GGA GTC CCT TCT CGC TTC TCT 270  
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser  
60 65

GGA	TCC	GGC	TCC	GGA	ACG	GAT	TAC	ACT	CTG	300
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	
				70					75	
ACC	ATC	AGC	AGT	CTG	CAA	CCT	GAG	GAC	TTC	330
Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	
				80					85	
GCT	ACG	TAT	TAC	TGT	CAG	AAC	GTT	TTA	AAT	360
Ala	Thr	Tyr	Tyr	Cys	Gln	Asn	Val	Leu	Asn	
				90					95	
ACT	CCG	TTG	ACT	TTC	GGA	CAG	GGT	ACC	AAG	390
Thr	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
				100					105	
GTG	GAA	ATA	AAA	CGA	ACT	GTG	GCT	GCA	CCA	420
Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	
				110					115	
TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAT	GAG	450
Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	
				120					125	
CAG	TTG	AAA	TCT	GGA	ACT	GCC	TCT	GTT	GTG	480
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	
				130					135	
TGC	CTG	CTG	AAT	AAC	TTC	TAT	CCC	AGA	GAG	510
Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	
				140					145	
GCC	AAA	GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	540
Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	
				150					155	
CTC	CAA	TCG	GGT	AAC	TCC	CAG	GAG	AGT	GTC	570
Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	
				160					165	
ACA	GAG	CAG	GAC	AGC	AAG	GAC	AGC	ACC	TAC	600
Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	
				170					175	
AGC	CTC	AGC	AGC	ACC	CTG	ACG	CTG	AGC	AAA	630
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
				180					185	
GCA	GAC	TAC	GAG	AAA	CAC	AAA	GTC	TAC	GCC	660
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	
				190					195	

TGT TAG 726  
Cys

(Humanized light chain)

GGC GCC AGC GAA AAC ATC TAT GGC GCG CTG 180  
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu  
30 35

AAC	TGG	TAT	CAA	CGT	AAA	CCT	GGG	AAA	GCT	210
Asn	Trp	Tyr	Gln	Arg	Lys	Pro	Gly	Lys	Ala	
				40					45	
CCG	AAG	CTT	CTG	ATT	TAC	GGT	GCG	ACG	AAC	240
Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Thr	Asn	
				50					55	
CTG	GCA	GAT	GGA	GTC	CCT	TCT	CGC	TTC	TCT	270
Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	
				60					65	
GGA	TCC	GGC	TCC	GGA	ACG	GAT	TTC	ACT	CTG	300
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	
				70					75	
ACC	ATC	AGC	AGT	CTG	CAG	CCT	GAA	GAC	TTC	330
Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	
				80					85	
GCT	ACG	TAT	TAC	TGT	CAG	AAC	GTT	TTA	AAT	360
Ala	Thr	Tyr	Tyr	Cys	Gln	Asn	Val	Leu	Asn	
				90					95	
ACT	CCG	TTG	ACT	TTC	GGA	CAG	GGT	ACC	AAG	390
Thr	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
				100					105	
GTG	GAA	ATA	AAA	CGA	ACT	GTG	GCT	GCA	CCA	420
Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	
				110					115	
TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAT	GAG	450
Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	
				120					125	
CAG	TTG	AAA	TCT	GGA	ACT	GCC	TCT	GTT	GTG	480
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	
				130					135	
TGC	CTG	CTG	AAT	AAC	TTC	TAT	CCC	AGA	GAG	510
Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	
				140					145	
GCC	AAA	GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	540
Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	
				150					155	
CTC	CAA	TCG	GGT	AAC	TCC	CAG	GAG	AGT	GTC	570
Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	
				160					165	

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600  
 Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr  
                   170                  175

AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630  
 Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
                   180                  185

GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC 660  
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
                   190                  195

TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG 690  
 Cys Glu Val Thr His Gln Gly Leu Ser Ser  
                   200                  205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720  
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu  
                   210                  215

TGT TAG  726  
 Cys

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1 VL + 012

(Humanized light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATG GAC ATG AGG GTC CCC GCT CAG CTC CTG 30  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu  
                   -20                  -15

GGG CTC CTG CTA CTC TGG CTC CGA GGT GCC 60  
 Gly Leu Leu Leu Leu Trp Leu Arg Gly Ala  
                   -10                  -5

AGA TGT GAT ATC CAG ATG ACC CAG TCC CCG 90  
 Arg Cys Asp Ile Gln Met Thr Gln Ser Pro  
                   1                  5

TCC	TCC	CTG	TCC	GCC	TCT	GTG	GGC	GAT	AGG	120
Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
	10					15				

GTC	ACC	ATC	ACC	TGC	GGC	GCC	AGC	GAA	AAC	150
Val	Thr	Ile	Thr	Cys	Gly	Ala	Ser	Glu	Asn	
	20					25				

ATC	TAT	GGC	GCG	CTG	AAC	TGG	TAT	CAA	CAG	180
Ile	Tyr	Gly	Ala	Leu	Asn	Trp	Tyr	Gln	Gln	
	30					35				

AAA	CCC	GGG	AAA	GCT	CCG	AAG	CTT	CTG	ATT	210
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
	40					45				

TAC	GGT	GCG	ACG	AAC	CTG	GCA	GAT	GGA	GTC	240
Tyr	Gly	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	
	50					55				

CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	270
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
	60					65				

ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	300
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
	70					75				

CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	330
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
	80					85				

CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	360
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
	90					95				

GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGA	390
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
	100					105				

ACT	GTG	GCT	GCA	CCA	TCT	GTC	TTC	ATC	TTC	420
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	
	110					115				

CCG	CCA	TCT	GAT	GAG	CAG	TTG	AAA	TCT	GGA	450
Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	
	120					125				

ACT	GCC	TCT	GTT	GTG	TGC	CTG	CTG	AAT	AAC	480
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	
	130					135				



TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG 510  
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
 140 145

AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC 540  
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
 150 155

TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC 570  
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
 160 165

AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC 600  
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr  
 170 175

CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 630  
 Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 180 185

CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT 660  
 His Lys Val Tyr Ala Cys Glu Val Thr His  
 190 195

CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC 690  
 Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 200 205

TTC AAC AGG GGA GAG TGT TAG 711  
 Phe Asn Arg Gly Glu Cys  
 210

- (2) INFORMATION FOR SEQ ID NO:16:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 750 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Other nucleic acid
    - (A) DESCRIPTION: 5G1.1 VH + IGHRD  
 (Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30  
 Met Lys Trp Ser Trp Val Ile Leu Phe Leu  
 -15 -10

CTG	TCA	GTA	ACT	GCC	GGC	GTC	CAC	TCC	CAA	60
Leu	Ser	Val	Thr	Ala	Gly	Val	His	Ser	Gln	
				-5					1	
GTC	CAA	CTG	GTG	CAA	TCC	GGC	GCC	GAG	GTC	90
Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	
			5					10		
AAG	AAG	CCA	GGG	GCC	TCA	GTC	AAA	GTG	TCC	120
Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	
			15					20		
TGT	AAA	GCT	AGC	GGC	TAT	ATT	TTT	TCT	AAT	150
Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Ser	Asn	
			25					30		
TAT	TGG	ATT	CAA	TGG	GTG	CGT	CAG	GCC	CCC	180
Tyr	Trp	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	
			35					40		
GGG	CAG	GGC	CTG	GAA	TGG	ATG	GGT	GAG	ATC	210
Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	
			45					50		
TTA	CCG	GGC	TCT	GGT	AGC	ACC	GAA	TAT	GCC	240
Leu	Pro	Gly	Ser	Gly	Ser	Thr	Glu	Tyr	Ala	
			55					60		
CAA	AAA	TTC	CAG	GGC	CGT	GTT	ACT	ATG	ACT	270
Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	
			65					70		
CGT	GAC	ACT	TCG	ACT	AGT	ACA	GTA	TAC	ATG	300
Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr	Met	
			75					80		
GAG	CTC	TCC	AGC	CTG	CGA	TCG	GAG	GAC	ACG	330
Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	
			85					90		
GCC	GTC	TAT	TAT	TGC	GCG	CGT	TAT	TTT	TTT	360
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	
			95					100		
GGT	TCT	AGC	CCG	AAT	TGG	TAT	TTT	GAT	GTT	390
Gly	Ser	Ser	Pro	Asn	Trp	Tyr	Phe	Asp	Val	
			105					110		

TGG	GGT	CAA	GGA	ACC	CTG	GTC	ACT	GTC	TCG	420
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
			115						120	
AGC	GCC	TCC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	450
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
			125						130	
CCC	CTG	GCG	CCC	TCC	TCC	AAG	AGC	ACC	TCT	480
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	
			135						140	
GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	GTC	510
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	
			145						150	
AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	540
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
			155						160	
TCG	TGG	AAC	TCA	GGC	GCC	CTG	ACC	AGC	GGC	570
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	
			165						170	
GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	600
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
			175						180	
TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	630
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	
			185						190	
ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG	660
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	
			195						200	
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	690
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
			205						210	
AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA	GTT	GAG	720
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	
			215						220	
CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TAA	750
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr		
			225						230	

- (2) INFORMATION FOR SEQ ID NO:17:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 747 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Other nucleic acid
    - (A) DESCRIPTION: 5G1.1 scFv D012  
(Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG	GCC	GAT	ATC	CAG	ATG	ACC	CAG	TCC	CCG	30
Met	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	
1				5					10	
TCC	TCC	CTG	TCC	GCC	TCT	GTG	GGC	GAT	AGG	60
Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
				15					20	
GTC	ACC	ATC	ACC	TGC	GGC	GCC	AGC	GAA	AAC	90
Val	Thr	Ile	Thr	Cys	Gly	Ala	Ser	Glu	Asn	
				25					30	
ATC	TAT	GGC	GCG	CTG	AAC	TGG	TAT	CAA	CAG	120
Ile	Tyr	Gly	Ala	Leu	Asn	Trp	Tyr	Gln	Gln	
				35					40	
AAA	CCT	GGG	AAA	GCT	CCG	AAG	CTT	CTG	ATT	150
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
				45					50	
TAC	GGT	GCG	ACG	AAC	CTG	GCA	GAT	GGA	GTC	180
Tyr	Gly	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	
				55					60	
CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	
ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	

CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	

GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	

ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	

TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	

GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	

GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	

AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	

CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	

CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	

TCT	GGT	AGC	ACC	GAA	TAT	GCC	CAA	AAA	TTC	570
Ser	Gly	Ser	Thr	Glu	Tyr	Ala	Gln	Lys	Phe	
				185					190	

CAG	GGC	CGT	GTT	ACT	ATG	ACG	CGT	GAC	ACT	600
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	
				195					200	

TCG	ACT	AGT	ACA	GTA	TAC	ATG	GAG	CTC	TCC	630
Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	
				205					210	

AGC	CTG	CGA	TCG	GAG	GAC	ACG	GCC	GTC	TAT	660
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	
				215					220	

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690  
 Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser  
                   225                  230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720  
 Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln  
                   235                  240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747  
 Gly Thr Leu Val Thr Val Ser Ser  
                   245

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5248 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: pET Trc S05/NI  
                   prokaryotic expression vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG 50  
 TGGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT 100  
 CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTTCCTCCG 150  
 TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT AGTGCTTTAC 200  
 GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG 250  
 CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT 300  
 CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACACTC AACCTATCT 350  
 CGGTCTATTC TTTTGATTTA TAAGGGATTT TGCCGATTTC GGCCTATTGG 400  
 TTAAAAAATG AGCTGATTTA ACAAAAATTT AACGCGAATT TTAACAAAAT 450  
 ATTAACGTTT ACAATTTTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA 500  
 CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG 550  
 AGACAATAAC CCTGATAAAT GCTTCAATAA TATTGAAAAA GGAAGAGTAT 600

GAGTATTCAA	CATTTCCGTG	TCGCCCTTAT	TCCCTTTTTT	GCGGCATTTT	650
GCCTTCCTGT	TTTTGCTCAC	CCAGAAACGC	TGGTGAAAGT	AAAAGATGCT	700
GAAGATCAGT	TGGGTGCACG	AGTGGGTAC	ATCGAACTGG	ATCTCAACAG	750
CGGTAAGATC	CTTGAGAGTT	TTCGCCCCGA	AGAACGTTTT	CCAATGATGA	800
GCACTTTTAA	AGTTCTGCTA	TGTGGCGCGG	TATTATCCCG	TATTGACGCC	850
GGGCAAGAGC	AACTCGGTCTG	CCGCATACAC	TATTCTCAGA	ATGACTTGGT	900
TGAGTACTCA	CCAGTCACAG	AAAAGCATCT	TACGGATGGC	ATGACAGTAA	950
GAGAATTATG	CAGTGCTGCC	ATAACCATGA	GTGATAACAC	TGCGGCCAAC	1000
TTACTTCTGA	CAACGATCGG	AGGACCGAAG	GAGCTAACCG	CTTTTTTGCA	1050
CAACATGGGG	GATCATGTAA	CTCGCCTTGA	TCGTTGGGAA	CCGGAGCTGA	1100
ATGAAGCCAT	ACCAAACGAC	GAGCGTGACA	CCACGATGCC	TGCAGCAATG	1150
GCAACAACGT	TGCGCAAAC	ATTAAC	TGGC	GAAC	1200
CCGGCAACAA	TTAATAGACT	GGATGGAGGC	GGATAAAGTT	GCAGGACCAC	1250
TTCTGCGCTC	GGCCCTTCCG	GCTGGCTGGT	TTATTGCTGA	TAAATCTGGA	1300
GCCGGTGAGC	GTGGGTCTCG	CGGTATCATT	GCAGCACTGG	GGCCAGATGG	1350
TAAGCCCTCC	CGTATCGTAG	TTATCTACAC	GACGGGGAGT	CAGGCAACTA	1400
TGGATGAACG	AAATAGACAG	ATCGCTGAGA	TAGGTGCCTC	ACTGATTAAG	1450
CATTGGTAAC	TGTCAGACCA	AGTTTACTCA	TATATACTTT	AGATTGATTT	1500
AAAAC	TTTCAT	TTTAATTTA	AAAGGATCTA	GGTGAAGATC	1550
ATCTCATGAC	CAAAATCCCT	TAACGTGAGT	TTTCGTTCCA	CTGAGCGTCA	1600
GACCCCGTAG	AAAAGATCAA	AGGATCTTCT	TGAGATCCTT	TTTTTCTGCG	1650
CGTAATCTGC	TGCTTGCAAA	CAAAAAAACC	ACCGCTACCA	GCGGTGGTTT	1700
GTTTGCCGGA	TCAAGAGCTA	CCAAC	TCTTT	TTCCGAAGGT	1750
AGCAGAGCGC	AGATACCAA	TACTGTCCTT	CTAGTGTAGC	CGTAGTTAGG	1800
CCACCACTTC	AAGAACTCTG	TAGCACCGCC	TACATACCTC	GCTCTGCTAA	1850
TCCTGTTACC	AGTGGCTGCT	GCCAGTGGCG	ATAAGTCGTG	TCTTACCGGG	1900

TTGGA	CTCAA	GACGATAGTT	ACCGGATAAG	GCGCAGCGGT	CGGGCTGAAC	1950
GGGGG	GTTCG	TGCACACAGC	CCAGCTTGGA	GCGAACGACC	TACACCGAAC	2000
TGAGATA	CTT	ACAGCGTGAG	CTATGAGAAA	GCGCCACGCT	TCCCGAAGGG	2050
AGAAAGG	CGG	ACAGGTATCC	GGTAAGCGGC	AGGGTCGGAA	CAGGAGAGCG	2100
CACGAGG	GAG	CTTCCAGGGG	GAAACGCCTG	GTATCTTTAT	AGTCCTGTCTG	2150
GGTTTCG	CCA	CCTCTGACTT	GAGCGTCGAT	TTTTGTGATG	CTCGTCAGGG	2200
GGGCGG	AGCC	TATGGAAAAA	CGCCAGCAAC	GCGGCCTTTT	TACGGTTCCT	2250
GGCCTTTT	TGC	TGGCCTTTTG	CTCACATGTT	CTTTCCTGCG	TTATCCCCTG	2300
ATTCTGT	GGA	TAACCGTATT	ACCGCCTTTG	AGTGAGCTGA	TACCGCTCGC	2350
CGCAGCC	GAA	CGACCGAGCG	CAGCGAGTCA	GTGAGCGAGG	AAGCGGAAGA	2400
GCGCCTG	ATG	CGGTATTTTC	TCCTTACGCA	TCTGTGCGGT	ATTTACACACC	2450
GCATATAT	G	TGCACTCTCA	GTACAATCTG	CTCTGATGCC	GCATAGTTAA	2500
GCCAGTATA	C	ACTCCGCTAT	CGCTACGTGA	CTGGGTCATG	GCTGCGCCCC	2550
GACACCC	GCC	AACACCCGCT	GACGCGCCCT	GACGGGCTTG	TCTGCTCCCG	2600
GCATCCG	CTT	ACAGACAAGC	TGTGACCGTC	TCCGGGAGCT	GCATGTGTCA	2650
GAGGTTTT	TCA	CCGTCATCAC	CGAAACGCGC	GAGGCAGCTG	CGGTAAAGCT	2700
CATCAGCG	TG	GTCGTGAAGC	GATTCACAGA	TGTCTGCCTG	TTCATCCGCG	2750
TCCAGCTC	GT	TGAGTTTCTC	CAGAAGCGTT	AATGTCTGGC	TTCTGATAAA	2800
GCGGGCC	ATG	TTAAGGGCGG	TTTTTTCCTG	TTTGGTCACT	GATGCCTCCG	2850
TGTAAGGG	G	ATTTCTGTTC	ATGGGGGTAA	TGATACCGAT	GAAACGAGAG	2900
AGGATGCT	CA	CGATACGGGT	TACTGATGAT	GAACATGCCC	GGTTACTGGA	2950
ACGTTGT	GAG	GGTAAACAAC	TGGCGGTATG	GATGCGGCGG	GACCAGAGAA	3000
AAATCACT	CA	GGGTCAATGC	CAGCGCTTCG	TTAATACAGA	TGTAGGTGTT	3050
CCACAGGG	TA	GCCAGCAGCA	TCCTGCGATG	CAGATCCGGA	ACATAATGGT	3100
GCAGGGC	GCT	GACTTCCGCG	TTTCCAGACT	TTACGAAACA	CGGAAACCGA	3150



AGACCATTCA	TGTTGTTGCT	CAGGTCGCAG	ACGTTTTTGCA	GCAGCAGTCG	3200
CTTCACGTTT	GCTCGCGTAT	CGGTGATTCA	TTCTGCTAAC	CAGTAAGGCA	3250
ACCCCGCCAG	CCTAGCCGGG	TCCTCAACGA	CAGGAGCACG	ATCATGCGCA	3300
CCCGTGGGGC	CGCCATGCCG	GCGATAATGG	CCTGCTTCTC	GCCGAAACGT	3350
TTGGTGGCGG	GACCAGTGAC	GAAGGCTTGA	GCGAGGGCGT	GCAAGATTCC	3400
GAATACCGCA	AGCGACAGGC	CGATCATCGT	CGCGCTCCAG	CGAAAGCGGT	3450
CCTCGCCGAA	AATGACCCAG	AGCGCTGCCG	GCACCTGTCC	TACGAGTTGC	3500
ATGATAAAGA	AGACAGTCAT	AAGTGCGGCG	ACGATAGTCA	TGCCCCGCGC	3550
CCACCGGAAG	GAGCTGACTG	GGTTGAAGGC	TCTCAAGGGC	ATCGGTTCGAG	3600
ATCCCGGTGC	CTAATGAGTG	AGCTAACTTA	CATTAATTGC	GTTGCGCTCA	3650
CTGCCCCGCTT	TCCAGTCGGG	AAACCTGTCT	TGCCAGCTGC	ATTAATGAAT	3700
CGGCCAACGC	GCGGGGAGAG	GCGGTTTGCG	TATTGGGCGC	CAGGGTGGTT	3750
TTTCTTTTCA	CCAGTGAGAC	GGGCAACAGC	TGATTGCCCT	TCACCGCCTG	3800
GCCCTGAGAG	AGTTGCAGCA	AGCGGTCCAC	GCTGGTTTGC	CCCAGCAGGC	3850
GAAAATCCTG	TTTGATGGTG	GTTAACGGCG	GGATATAACA	TGAGCTGTCT	3900
TCGGTATCGT	CGTATCCAC	TACCGAGATA	TCCGCACCAA	CGCGCAGCCC	3950
GGACTCGGTA	ATGGCGCGCA	TTGCGCCCAG	CGCCATCTGA	TCGTTGGCAA	4000
CCAGCATCGC	AGTGGGAACG	ATGCCCTCAT	TCAGCATTTG	CATGGTTTGT	4050
TGAAAACCGG	ACATGGCACT	CCAGTCGCCT	TCCCGTTCCG	CTATCGGCTG	4100
AATTTGATTG	CGAGTGAGAT	ATTTATGCCA	GCCAGCCAGA	CGCAGACGCG	4150
CCGAGACAGA	ACTTAATGGG	CCCGCTAACA	GCGCGATTTG	CTGGTGACCC	4200
AATGCGACCA	GATGCTCCAC	GCCCAGTCGC	GTACCGTCTT	CATGGGAGAA	4250
AATAATACTG	TTGATGGGTG	TCTGGTCAGA	GACATCAAGA	AATAACGCCG	4300
GAACATTAGT	GCAGGCAGCT	TCCACAGCAA	TGGCATCCTG	GTCATCCAGC	4350
GGATAGTTAA	TGATCAGCCC	ACTGACGCGT	TGCGCGAGAA	GATTGTGCAC	4400
CGCCGCTTTA	CAGGCTTCGA	CGCCGCTTCG	TTCTACCATC	GACACCACCA	4450

CGCTGGCACC	CAGTTGATCG	GCGCGAGATT	TAATCGCCGC	GACAATTTGC	4500
GACGGCGCGT	GCAGGGCCAG	ACTGGAGGTG	GCAACGCCAA	TCAGCAACGA	4550
CTGTTTGCCC	GCCAGTTGTT	GTGCCACGCG	GTTGGGAATG	TAATTCAGCT	4600
CCGCCATCGC	CGCTTCCACT	TTTTCCCGCG	TTTTCGCAGA	AACGTGGCTG	4650
GCCTGGTTCA	CCACGCGGGA	AACGGTCTGA	TAAGAGACAC	CGGCATACTC	4700
TGCGACATCG	TATAACGTTA	CTGGTTTCAC	ATTCACCACC	CTGAATTGAC	4750
TCTCTTCCGG	GCGCTATCAT	GCCATACCGC	GAAAGGTTTT	GCGCCATTCG	4800
ATGGTGTCCG	GGATCTCGAC	GCTCTCCCTT	ATGCGACTCC	TGCATTAGGA	4850
AGCAGCCCAG	TAGTAGGTTG	AGGCCGTTGA	GCACCGCCGC	CGCAAGGAAT	4900
GGTGCATGCG	GTACCAGCTG	TTGACAATTA	ATCATCCGGC	TCGTATAATA	4950
GTACTGTGTG	GAATTGTGAG	CGCTCACAAT	TCCACACATC	TAGAAATAAT	5000
TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGGAGATCTG	GATCCATCGA	5050
TGAATTCGAG	CTCCGTCGAC	AAGCTTGCGG	CCGCACTCGA	GCACCACCAC	5100
CACCACCACT	GAGATCCGGC	TGCTAACAAA	GCCCGAAAGG	AAGCTGAGTT	5150
GGCTGCTGCC	ACCGCTGAGC	AATAACTAGC	ATAACCCCTT	GGGGCCTCTA	5200
AACGGGTCTT	GAGGGGTTTT	TTGCTGAAAG	GAGGAACTAT	ATCCGGAT	5248

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: N19/8 scFv (His Tagged)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG	GCC	AAT	ATT	GTG	CTG	ACC	CAA	TCT	CCA	30
Met	Ala	Asn	Ile	Val	Leu	Thr	Gln	Ser	Pro	
1				5					10	
GCT	TCT	TTG	GCT	GTG	TCT	CTA	GGG	CAG	AGG	60
Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	
				15					20	
GCC	ACC	ATA	TCC	TGC	AGA	GCC	AGT	GAA	AGT	90
Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	Ser	
				25					30	
GTT	GAT	AGT	TAT	GAC	AAT	AGT	TTT	ATG	CAC	120
Val	Asp	Ser	Tyr	Asp	Asn	Ser	Phe	Met	His	
				35					40	
TGG	TAC	CAG	CAG	AAA	CCA	GGA	CAG	CCA	CCC	150
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	
				45					50	
AAA	CTC	CTC	ATC	TTT	CTT	GCA	TCC	AAC	CTA	180
Lys	Leu	Leu	Ile	Phe	Leu	Ala	Ser	Asn	Leu	
				55					60	
GAA	TCT	GGG	GTC	CCT	GCC	AGG	TTC	AGT	GGC	210
Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	
				65					70	
AGT	GGG	TCT	AGG	ACA	GAC	TTC	ACC	CTC	ACC	240
Ser	Gly	Ser	Arg	Thr	Asp	Phe	Thr	Leu	Thr	
				75					80	
ATT	GAT	CCT	GTG	GAG	GCT	GAT	GAT	GCT	GCA	270
Ile	Asp	Pro	Val	Glu	Ala	Asp	Asp	Ala	Ala	
				85					90	
ACC	TAT	TAC	TGT	CAG	CAA	AAT	AAT	GAG	GTT	300
Thr	Tyr	Tyr	Cys	Gln	Gln	Asn	Asn	Glu	Val	
				95					100	

CCG	AAC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	330
Pro	Asn	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	
				105					110	
GAA	ATA	AAA	CGG	ACC	GGA	GGT	GGC	GGG	TCG	360
Glu	Ile	Lys	Arg	Thr	Gly	Gly	Gly	Gly	Ser	
				115					120	
GGT	GGC	GGG	GGA	TCG	GGT	GGC	GGA	GGG	TCG	390
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
				125					130	
GAC	GTC	AAG	CTC	GTG	GAG	TCT	GGG	GGA	GAC	420
Asp	Val	Lys	Leu	Val	Glu	Ser	Gly	Gly	Asp	
				135					140	
TTA	GTG	AAG	CTT	GGA	GGG	TCC	CTG	AAA	CTC	450
Leu	Val	Lys	Leu	Gly	Gly	Ser	Leu	Lys	Leu	
				145					150	
TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACC	TTC	AGT	480
Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	
				155					160	
AGC	TAT	TAT	ATG	TCT	TGG	GTT	CGC	CAG	ATT	510
Ser	Tyr	Tyr	Met	Ser	Trp	Val	Arg	Gln	Ile	
				165					170	
TCA	GAG	AAG	AGG	CTG	GAG	TTG	GTC	GCA	GCC	540
Ser	Glu	Lys	Arg	Leu	Glu	Leu	Val	Ala	Ala	
				175					180	
ATT	AAT	AGT	AAT	GGT	GAT	AGC	ACC	TAC	TAT	570
Ile	Asn	Ser	Asn	Gly	Asp	Ser	Thr	Tyr	Tyr	
				185					190	
CCA	GAC	ACT	GTG	AAG	GGC	CGA	TTC	ACC	ATC	600
Pro	Asp	Thr	Val	Lys	Gly	Arg	Phe	Thr	Ile	
				195					200	
TCC	AGA	GAC	AAT	GCC	AAG	AGC	ACC	CTG	GAT	630
Ser	Arg	Asp	Asn	Ala	Lys	Ser	Thr	Leu	Asp	
				205					210	
CTG	CAA	ATG	AGC	AGT	CTG	AAG	TCT	GAG	GAC	660
Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	
				215					220	

ACA GCC TTG TAT TTC TGT GTA AGA GAG ACT 690  
 Thr Ala Leu Tyr Phe Cys Val Arg Glu Thr  
 225 230

TAT TAC TAC GGG ATT AGT CCC GTC TTC GAT 720  
 Tyr Tyr Tyr Gly Ile Ser Pro Val Phe Asp  
 235 240

GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC 750  
 Val Trp Gly Thr Gly Thr Thr Val Thr Val  
 245 250

TCC TCA CTC GAG CAC CAC CAC CAC CAC CAC 780  
 Ser Ser Leu Glu His His His His His His  
 255 260

TGA 783

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1 scFv C012 (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30  
 Met Ala Asp Ile Gln Met Thr Gln Ser Pro  
 1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60  
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 15 20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90  
 Val Thr Ile Thr Cys Gly Ala Ser Glu Asn  
 25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120  
 Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln  
 35 40

AAA CCC GGG AAA GCT CCG AAG CTT CTG ATT 150  
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 45 50

TAC	GGT	GCG	ACG	AAC	CTG	GCA	GAT	GGA	GTC	180
Tyr	Gly	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	
				55					60	

CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	

ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	

CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	

CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	

GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	

ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	

TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	

GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	

GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	

AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	

CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	

CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	

TCT	GGT	AGC	ACC	GAA	TAT	ACC	GAA	AAT	TTT	570
Ser	Gly	Ser	Thr	Glu	Tyr	Thr	Glu	Asn	Phe	
				185					190	

AAA	GAC	CGT	GTT	ACT	ATG	ACG	CGT	GAC	ACT	600
Lys	Asp	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	
				195					200	

TCG	ACT	AGT	ACA	GTA	TAC	ATG	GAG	CTC	TCC	630
Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	
				205					210	

AGC	CTG	CGA	TCG	GAG	GAC	ACG	GCC	GTC	TAT	660
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	
				215					220	

TAT	TGC	GCG	CGT	TAT	TTT	TTT	GGT	TCT	AGC	690
Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	Gly	Ser	Ser	
				225					230	

CCG	AAT	TGG	TAT	TTT	GAT	GTT	TGG	GGT	CAA	720
Pro	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	
				235					240	

GGA	ACC	CTG	GTC	ACT	GTC	TCG	AGC	TGA		747
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
				245						

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG Met 1	GCC Ala	GAT Asp	ATC Ile	CAG Gln 5	ATG Met	ACC Thr	CAG Gln	TCC Ser	CCG Pro 10	30
TCC Ser	TCC Ser	CTG Leu	TCC Ser	GCC Ala 15	TCT Ser	GTG Val	GGC Gly	GAT Asp	AGG Arg 20	60
GTC Val	ACC Thr	ATC Ile	ACC Thr	TGC Cys 25	CGT Arg	GCT Ala	AGC Ser	GAA Glu	AAC Asn 30	90
ATC Ile	TAT Tyr	GGC Gly	GCG Ala	CTG Leu 35	AAC Asn	TGG Trp	TAT Tyr	CAA Gln	CAG Gln 40	120
AAA Lys	CCT Pro	GGG Gly	AAA Lys	GCT Ala 45	CCG Pro	AAG Lys	CTT Leu	CTG Leu	ATT Ile 50	150
TAC Tyr	GGT Gly	GCG Ala	ACG Thr	AAC Asn 55	CTG Leu	GCA Ala	GAT Asp	GGA Gly	GTC Val 60	180
CCT Pro	TCT Ser	CGC Arg	TTC Phe	TCT Ser 65	GGA Gly	TCC Ser	GGC Gly	TCC Ser	GGA Gly 70	210
ACG Thr	GAT Asp	TTC Phe	ACT Thr	CTG Leu 75	ACC Thr	ATC Ile	AGC Ser	AGT Ser	CTG Leu 80	240
CAG Gln	CCT Pro	GAA Glu	GAC Asp	TTC Phe 85	GCT Ala	ACG Thr	TAT Tyr	TAC Tyr	TGT Cys 90	270



CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	

GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	

ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	

TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	

GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	

GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	

AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	

CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	

CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	

TCT	GGT	AGC	ACC	GAA	TAT	GCC	CAA	AAA	TTC	570
Ser	Gly	Ser	Thr	Glu	Tyr	Ala	Gln	Lys	Phe	
				185					190	

CAG	GGC	CGT	GTT	ACT	ATG	ACG	CGT	GAC	ACT	600
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	
				195					200	

TCG	ACT	AGT	ACA	GTA	TAC	ATG	GAG	CTC	TCC	630
Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	
				205					210	

AGC	CTG	CGA	TCG	GAG	GAC	ACG	GCC	GTC	TAT	660
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	
				215					220	

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690  
 Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser  
                   225                  230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720  
 Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln  
                   235                  240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747  
 Gly Thr Leu Val Thr Val Ser Ser  
                   245

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv D012C  
 (Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30  
 Met Ala Asp Ile Gln Met Thr Gln Ser Pro  
   1                  5                  10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60  
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
                   15                  20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90  
 Val Thr Ile Thr Cys Gly Ala Ser Glu Asn  
                   25                  30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120  
 Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln  
                   35                  40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150  
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   45                  50

TAC GGT GCG ACG AGC CTG CAG TCT GGA GTC 180  
 Tyr Gly Ala Thr Ser Leu Gln Ser Gly Val  
                   55                  60

CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	
ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	
CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	
GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	
ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	
TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	
GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	
GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	
AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	
CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	
CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	

TCT GGT AGC ACC GAA TAT GCC CAA AAA TTC 570  
 Ser Gly Ser Thr Glu Tyr Ala Gln Lys Phe  
 185 190

CAG GGC CGT GTT ACT ATG ACG CGT GAC ACT 600  
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr  
 195 200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630  
 Ser Thr Ser Thr Val Tyr Met Glu Leu Ser  
 205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660  
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
 215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690  
 Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser  
 225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720  
 Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln  
 235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747  
 Gly Thr Leu Val Thr Val Ser Ser  
 245

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv D012D  
 (Humanized scFv)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30  
 Met Ala Asp Ile Gln Met Thr Gln Ser Pro  
 1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60  
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 15 20

GTC	ACC	ATC	ACC	TGC	CGT	GCT	AGC	GAA	AAC	90
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Asn	
				25					30	
ATC	TAT	GGC	GCG	CTG	AAC	TGG	TAT	CAA	CAG	120
Ile	Tyr	Gly	Ala	Leu	Asn	Trp	Tyr	Gln	Gln	
				35					40	
AAA	CCT	GGG	AAA	GCT	CCG	AAG	CTT	CTG	ATT	150
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
				45					50	
TAC	GGT	GCG	ACG	AGC	CTG	CAG	TCT	GGA	GTC	180
Tyr	Gly	Ala	Thr	Ser	Leu	Gln	Ser	Gly	Val	
				55					60	
CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	
ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	
CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	
GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	
ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	
TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	
GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	

GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	
AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	
CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	
CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	
TCT	GGT	AGC	ACC	GAA	TAT	GCC	CAA	AAA	TTC	570
Ser	Gly	Ser	Thr	Glu	Tyr	Ala	Gln	Lys	Phe	
				185					190	
CAG	GGC	CGT	GTT	ACT	ATG	ACG	CGT	GAC	ACT	600
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	
				195					200	
TCG	ACT	AGT	ACA	GTA	TAC	ATG	GAG	CTC	TCC	630
Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	
				205					210	
AGC	CTG	CGA	TCG	GAG	GAC	ACG	GCC	GTC	TAT	660
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	
				215					220	
TAT	TGC	GCG	CGT	TAT	TTT	TTT	GGT	TCT	AGC	690
Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	Gly	Ser	Ser	
				225					230	
CCG	AAT	TGG	TAT	TTT	GAT	GTT	TGG	GGT	CAA	720
Pro	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	
				235					240	
GGA	ACC	CTG	GTC	ACT	GTC	TCG	AGC	TGA		747
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
				245						

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 scFv C013 (humanized)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG	GCC	GAT	ATC	CAG	ATG	ACC	CAG	TCC	CCG	30
Met	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	
1				5					10	
TCC	TCC	CTG	TCC	GCC	TCT	GTG	GGC	GAT	AGG	60
Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
				15					20	
GTC	ACC	ATC	ACC	TGC	CGT	GCT	AGC	GAA	AAC	90
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Asn	
				25					30	
ATC	TAT	GGC	GCG	CTG	AAC	TGG	TAT	CAA	CAG	120
Ile	Tyr	Gly	Ala	Leu	Asn	Trp	Tyr	Gln	Gln	
				35					40	
AAA	CCC	GGG	AAA	GCT	CCG	AAG	CTT	CTG	ATT	150
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
				45					50	
TAC	GGT	GCG	ACG	AAC	CTG	GCA	GAT	GGA	GTC	180
Tyr	Gly	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	
				55					60	
CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	
ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	
CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	

GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	
ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	
TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	
GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	
GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	
AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	
CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	
CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	
TCT	GGT	AGC	ACC	GAA	TAT	ACC	GAA	AAT	TTT	570
Ser	Gly	Ser	Thr	Glu	Tyr	Thr	Glu	Asn	Phe	
				185					190	
AAA	GAC	CGT	GTT	ACT	ATG	ACG	CGT	GAC	ACT	600
Lys	Asp	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	
				195					200	
TCG	ACT	AGT	ACA	GTA	TAC	ATG	GAG	CTC	TCC	630
Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	
				205					210	
AGC	CTG	CGA	TCG	GAG	GAC	ACG	GCC	GTC	TAT	660
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	
				215					220	
TAT	TGC	GCG	CGT	TAT	TTT	TTT	GGT	TCT	AGC	690
Tyr	Cys	Ala	Arg	Tyr	Phe	Phe	Gly	Ser	Ser	
				225					230	



CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720  
 Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln  
                   235                  240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747  
 Gly Thr Leu Val Thr Val Ser Ser  
                   245

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION:5G1.1 scFv C014 (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30  
 Met Ala Asp Ile Gln Met Thr Gln Ser Pro  
   1                  5                  10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60  
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
                   15                  20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90  
 Val Thr Ile Thr Cys Gly Ala Ser Glu Asn  
                   25                  30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120  
 Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln  
                   35                  40

AAA CCC GGG AAA GCT CCG AAG CTT CTG ATT 150  
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   45                  50

TAC GGT GCG ACG AGC CTG CAG TCT GGA GTC 180  
 Tyr Gly Ala Thr Ser Leu Gln Ser Gly Val  
                   55                  60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210  
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
                   65                  70

ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	
CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	
GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	
ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	
TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	
GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	
GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	
AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	
CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	
CTG	GAA	TGG	ATG	GGT	GAG	ATC	TTA	CCG	GGC	540
Leu	Glu	Trp	Met	Gly	Glu	Ile	Leu	Pro	Gly	
				175					180	
TCT	GGT	AGC	ACC	GAA	TAT	ACC	GAA	AAT	TTT	570
Ser	Gly	Ser	Thr	Glu	Tyr	Thr	Glu	Asn	Phe	
				185					190	
AAA	GAC	CGT	GTT	ACT	ATG	ACG	CGT	GAC	ACT	600
Lys	Asp	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	
				195					200	

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630  
 Ser Thr Ser Thr Val Tyr Met Glu Leu Ser  
 205 210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660  
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
 215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690  
 Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser  
 225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720  
 Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln  
 235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747  
 Gly Thr Leu Val Thr Val Ser Ser  
 245

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1 scFv C015 (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30  
 Met Ala Asp Ile Gln Met Thr Gln Ser Pro  
 1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60  
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
 15 20

GTC ACC ATC ACC TGC CGT GCT AGC GAA AAC 90  
 Val Thr Ile Thr Cys Arg Ala Ser Glu Asn  
 25 30

ATC TAT GGC GCG CTG AAC TGG TAT CAA CAG 120  
 Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln  
 35 40

AAA	CCC	GGG	AAA	GCT	CCG	AAG	CTT	CTG	ATT	150
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
				45					50	
TAC	GGT	GCG	ACG	AGC	CTG	CAG	TCT	GGA	GTC	180
Tyr	Gly	Ala	Thr	Ser	Leu	Gln	Ser	Gly	Val	
				55					60	
CCT	TCT	CGC	TTC	TCT	GGA	TCC	GGC	TCC	GGA	210
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
				65					70	
ACG	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	CTG	240
Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	
				75					80	
CAG	CCT	GAA	GAC	TTC	GCT	ACG	TAT	TAC	TGT	270
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
				85					90	
CAG	AAC	GTT	TTA	AAT	ACT	CCG	TTG	ACT	TTC	300
Gln	Asn	Val	Leu	Asn	Thr	Pro	Leu	Thr	Phe	
				95					100	
GGA	CAG	GGT	ACC	AAG	GTG	GAA	ATA	AAA	CGT	330
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
				105					110	
ACT	GGC	GGT	GGT	GGT	TCT	GGT	GGC	GGT	GGA	360
Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
				115					120	
TCT	GGT	GGT	GGC	GGT	TCT	CAA	GTC	CAA	CTG	390
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	
				125					130	
GTG	CAA	TCC	GGC	GCC	GAG	GTC	AAG	AAG	CCA	420
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
				135					140	
GGG	GCC	TCA	GTC	AAA	GTG	TCC	TGT	AAA	GCT	450
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	
				145					150	
AGC	GGC	TAT	ATT	TTT	TCT	AAT	TAT	TGG	ATT	480
Ser	Gly	Tyr	Ile	Phe	Ser	Asn	Tyr	Trp	Ile	
				155					160	
CAA	TGG	GTG	CGT	CAG	GCC	CCC	GGG	CAG	GGC	510
Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				165					170	

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540  
 Leu Glu Trp Met Gly Glu Ile Leu Pro Gly  
                     175                    180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570  
 Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe  
                     185                    190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600  
 Lys Asp Arg Val Thr Met Thr Arg Asp Thr  
                     195                    200

TCG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630  
 Ser Thr Ser Thr Val Tyr Met Glu Leu Ser  
                     205                    210

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660  
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
                     215                    220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690  
 Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser  
                     225                    230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720  
 Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln  
                     235                    240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747  
 Gly Thr Leu Val Thr Val Ser Ser  
                     245

B<sup>1</sup>  
 Anal.